

SEQUENCE LISTING

<110> Duke-Cohan, Jonathan S.
Schlossman, Stuart F.

<120> REGULATION OF IMMUNE RESPONSES BY ATTRACTIN

<130> 00530-089002

<140> US 09/787,097

<141> 2001-03-13

<150> PCT/US99/20948

<151> 1999-09-14

<150> US 60/100,137

<151> 1998-09-14

<160> 25

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 3597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (3594)

<400> 1

atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg	48
Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr	
1 5 10 15	
gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgt gtc	96
Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val	
20 25 30	
aac ggc ggt cgc tgc aac cct ggc acc ggc cag tgc gtc tgc ccc gcc	144
Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala	
35 40 45	
ggc tgg gtg ggc gag caa tgc cag cac tgc ggg ggc cgc ttc aga cta	192
Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu	
50 55 60	
act gga tct tct ggg ttt gtg aca gat gga cct gga aat tat aaa tac	240
Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr	
65 70 75 80	
aaa acg aag tgc acg tgg ctc att gaa gga cag cca aat aga ata atg	288
Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met	
85 90 95	

aga ctt cgt ttc aat cat ttt gct aca gag tgt agt tgg gac cat tta	336
Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu	
100 105 110	
tat gtt tat gat ggg gac tca att tat gca ccg cta gtt gct gca ttt	384
Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe	
115 120 125	
agt ggc ctc att gtt cct gag aga gat ggc aat gag act gtc cct gag	432
Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu	
130 135 140	
gtt gtt gcc aca tca ggt tat gcc ttg ctg cat ttt ttt agt gat gct	480
Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala	
145 150 155 160	
gct tat aat ttg act gga ttt aat att act tac agt ttt gat atg tgt	528
Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys	
165 170 175	
cca aat aac tgc tca ggc cga gga gag tgt aag atc agt aat agc agc	576
Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser	
180 185 190	
gat act gtt gaa tgt gaa tgt tct gaa aac tgg aaa ggt gaa gca tgt	624
Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys	
195 200 205	
gac att cct cac tgt aca gac aac tgt ggt ttt cct cat cga ggc atc	672
Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile	
210 215 220	
tgc aat tca agt gat gtc aga gga tgc tcc tgc ttc tca gac tgg cag	720
Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln	
225 230 235 240	
ggc cct gga tgt tca gtt cct gta cca gct aac cag tca ttt tgg act	768
Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr	
245 250 255	
cga gag gaa tat tct aac tta aag ctc ccc aga gca tct cat aaa gct	816
Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala	
260 265 270	
gtg gtc aat gga aac att atg tgg gtt gtt gga gga tat atg ttc aac	864
Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn	
275 280 285	
cac tca gat tat aac atg gtt cta gcg tat gac ctt gct tct agg gag	912
His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu	
290 295 300	
tgg ctt cca cta aac cgt tct gtg aac aat gtg gtt gtt aga tat ggt	960
Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly	
305 310 315 320	
cat tct ttg gca tta tac aag gat aaa att tac atg tat gga gga aaa	1008

His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys	
325 330 335	
att gat tca act ggg aat gtg acc aat gag ttg aga gtt ttt cac att	1056
Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile	
340 345 350	
cat aat gag tca tgg gtg ttg ttg acc cct aag gca aag gag cag tat	1104
His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr	
355 360 365	
gca gtg gtt ggg cac tct gca cac att gtt aca ctg aag aat ggc cga	1152
Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg	
370 375 380	
gtg gtc atg ctg gtc atc ttt ggt cac tgc cct ctc tat gga tat ata	1200
Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile	
385 390 395 400	
agc aat gtg cag gaa tat gat ttg gat aag aac aca tgg agt ata tta	1248
Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu	
405 410 415	
cac acc cag ggt gcc ctt gtg caa ggg ggt tac ggc cat agc agt gtt	1296
His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val	
420 425 430	
tac gac cat agg acc agg gcc cta tac gtt cat ggt ggc tac aag gct	1344
Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala	
435 440 445	
ttc agt gcc aat aag tac cgg ctt gca gat gat ctc tac cga tat gat	1392
Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp	
450 455 460	
gtg gat acc cag atg tgg acc att ctt aag gac agc cga ttt ttc cgt	1440
Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg	
465 470 475 480	
tac ttg cac aca gct gtg ata gtg agt gga acc atg ctg gtg ttt ggg	1488
Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly	
485 490 495	
gga aac aca cac aat gac aca tct atg agc cat ggc gcc aaa tgc ttc	1536
Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe	
500 505 510	
tct tca gat ttc atg gcc tat gac att gcc tgt gac cgc tgg tca gtg	1584
Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val	
515 520 525	
ctt ccc aga cct gat tcc acc atg atg tca aca gat ttg gcc att cca	1632
Leu Pro Arg Pro Asp Ser Thr Met Met Ser Thr Asp Leu Ala Ile Pro	
530 535 540	
gca gtc tta cac aac agc acc atg tat gtg ttc ggt ggt ttc aat agt	1680
Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser	

545	550	555	560	
ctc ctc ctc agc gac atc ctg gta ttc acc tcg gaa cag tgt gat gcg Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala 565 570 575				1728
cat cgg agt gaa gcc gct tgt tta gca gca gga cct ggt att cgg tgt His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys 580 585 590				1776
gtg tgg aac aca ggg tcg tct cag tgt atc tcg tgg gcg ctg gca act Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr 595 600 605				1824
gat gaa caa gaa gaa aag tta aaa tca gaa tgt ttt tcc aaa aga act Asp Glu Gln Glu Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr 610 615 620				1872
ctt gac cat gac aga tgt gac cag cac aca gat tgt tac agc tgc aca Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr 625 630 635 640				1920
gcc aac acc aat gac tgc cac tgg tgc aat gac cat tgt gtc ccc agg Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg 645 650 655				1968
aac cac agc tgc tca gaa ggc cag atc tcc att ttt agg tat gag aat Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn 660 665 670				2016
tgc ccc aag gat aac cct atg tac tac tgt aac aag aag acc agc tgc Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys 675 680 685				2064
agg agc tgt gcc ctg gac cag aac tgc cag tgg gag ccc cgg aat cag Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln 690 695 700				2112
gag tgc att gcc ctg ccc gaa aat atc tgt ggc att ggc tgg cat ttg Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu 705 710 715 720				2160
gtt gga aac tca tgt ttg aaa att act act gcc aag gag aat tat gac Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp 725 730 735				2208
aat gct aaa ttg ttc tgt agg aac cac aat gcc ctt ttg gct tct ctt Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu 740 745 750				2256
aca acc cag aag aag gta gaa ttt gtc ctt aag cag ctg cga ata atg Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met 755 760 765				2304
cag tca tct cag agc atg tcc aag ctc acc tta acc cca tgg gtc ggc Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly 770 775 780				2352

ctt cgg aag atc aat gtg tcc tac tgg tgc tgg gaa gat atg tcc cca	2400
Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro	
785 790 795 800	
ttt aca aat agt tta cta cag tgg atg ccg tct gag ccc agt gat gct	2448
Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala	
805 810 815	
gga ttc tgt gga att tta tca gaa ccc agt act cgg gga ctg aag gct	2496
Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala	
820 825 830	
gca acc tgc atc aac cca ctc aat ggt agt gtc tgt gaa agg cct gca	2544
Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala	
835 840 845	
aac cac agt gct aag cag tgc cgg aca cca tgt gcc ttg agg aca gca	2592
Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala	
850 855 860	
tgt gga gat tgc acc agc ggc agc tct gag tgc atg tgg tgc agc aac	2640
Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn	
865 870 875 880	
atg aag cag tgt gtg gac tcc aat gcc tat gtg gcc tcc ttc cct ttt	2688
Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe	
885 890 895	
ggc cag tgt atg gaa tgg tat acg atg agc acc tgc ccc cct gaa aat	2736
Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn	
900 905 910	
tgt tca ggc tac tgt acc tgt agt cat tgc ttg gag caa cca ggc tgt	2784
Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys	
915 920 925	
ggc tgg tgt act gat ccc agc aat act ggc aaa ggg aaa tgc ata gag	2832
Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu	
930 935 940	
ggt tcc tat aaa gga cca gtg aag atg cct tcg caa gcc cct aca gga	2880
Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly	
945 950 955 960	
aat ttc tat cca cag ccc ctg ctc aat tcc agc atg tgt cta gag gac	2928
Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp	
965 970 975	
agc aga tac aac tgg tct ttc att cac tgt cca gct tgc caa tgc aac	2976
Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn	
980 985 990	
ggc cac agt aaa tgc atc aat cag agc atc tgt gag aag tgt gag aac	3024
Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn	
995 1000 1005	

ctg acc aca ggc aag cac tgc gag acc tgc ata tct ggc ttc tac ggt 3072
 Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly
 1010 1015 1020
 gat ccc acc aat gga ggg aaa tgt cag cca tgc aag tgc aat ggg cac 3120
 Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His
 1025 1030 1035 1040
 gcg tct ctg tgc aac acc aac acg ggc aag tgc ttc tgc acc acc aag 3168
 Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys
 1045 1050 1055
 ggc gtc aag ggg gac gag tgc cag cta tgt gag gta gaa aat cga tac 3216
 Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr
 1060 1065 1070
 caa gga aac cct ctc aga gga aca tgt tat tat act ctt ctt att gac 3264
 Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp
 1075 1080 1085
 tat cag ttc acc ttt agt cta tcc cag gaa gat gat cgc tat tac aca 3312
 Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr
 1090 1095 1100
 gct atc aat ttt gtg gct act cct gac gaa caa aac agg gat ttg gac 3360
 Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp
 1105 1110 1115 1120
 atg ttc atc aat gcc tcc aag aat ttc aac ctc aac atc acc tgg gct 3408
 Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala
 1125 1130 1135
 gcc agt ttc tca gct gga acc cag gct gga gaa gag atg cct gtt gtt 3456
 Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val
 1140 1145 1150
 tca aaa acc aac att aag gag tac aaa gat agt ttc tct aat gag aag 3504
 Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys
 1155 1160 1165
 ttt gat ttt cgc aac cac cca aat atc act ttc ttt gtt tat gtc agt 3552
 Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser
 1170 1175 1180
 aat ttc acc tgg ccc atc aaa att cag gtg caa act gaa caa 3594
 Asn Phe Thr Trp Pro Ile Lys Ile Gln Val Gln Thr Glu Gln
 1185 1190 1195
 tga 3597
 <210> 2
 <211> 1198
 <212> PRT
 <213> Homo sapiens
 <400> 2
 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr

1	5	10	15
Ala Ala Thr	Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val		
	20	25	30
Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala			
	35	40	45
Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu			
	50	55	60
Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr			
	65	70	75
Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met			
	85	90	95
Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu			
	100	105	110
Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe			
	115	120	125
Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu			
	130	135	140
Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala			
	145	150	155
Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys			
	165	170	175
Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser			
	180	185	190
Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys			
	195	200	205
Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile			
	210	215	220
Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln			
	225	230	235
Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr			
	245	250	255
Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala			
	260	265	270
Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn			
	275	280	285
His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu			
	290	295	300
Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly			
	305	310	315
His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys			
	325	330	335
Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile			
	340	345	350
His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr			
	355	360	365
Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg			
	370	375	380
Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile			
	385	390	395
Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu			
	405	410	415
His Thr Gln Gly Ala Leu Val Gln Gly Gly Tyr Gly His Ser Ser Val			
	420	425	430
Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala			
	435	440	445
Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp			
	450	455	460

Val	Asp	Thr	Gln	Met	Trp	Thr	Ile	Leu	Lys	Asp	Ser	Arg	Phe	Phe	Arg
465					470					475					480
Tyr	Leu	His	Thr	Ala	Val	Ile	Val	Ser	Gly	Thr	Met	Leu	Val	Phe	Gly
				485					490						495
Gly	Asn	Thr	His	Asn	Asp	Thr	Ser	Met	Ser	His	Gly	Ala	Lys	Cys	Phe
			500					505					510		
Ser	Ser	Asp	Phe	Met	Ala	Tyr	Asp	Ile	Ala	Cys	Asp	Arg	Trp	Ser	Val
		515					520					525			
Leu	Pro	Arg	Pro	Asp	Ser	Thr	Met	Met	Ser	Thr	Asp	Leu	Ala	Ile	Pro
	530					535					540				
Ala	Val	Leu	His	Asn	Ser	Thr	Met	Tyr	Val	Phe	Gly	Gly	Phe	Asn	Ser
545				550						555					560
Leu	Leu	Leu	Ser	Asp	Ile	Leu	Val	Phe	Thr	Ser	Glu	Gln	Cys	Asp	Ala
				565					570					575	
His	Arg	Ser	Glu	Ala	Ala	Cys	Leu	Ala	Ala	Gly	Pro	Gly	Ile	Arg	Cys
			580					585					590		
Val	Trp	Asn	Thr	Gly	Ser	Ser	Gln	Cys	Ile	Ser	Trp	Ala	Leu	Ala	Thr
		595					600					605			
Asp	Glu	Gln	Glu	Glu	Lys	Leu	Lys	Ser	Glu	Cys	Phe	Ser	Lys	Arg	Thr
	610					615					620				
Leu	Asp	His	Asp	Arg	Cys	Asp	Gln	His	Thr	Asp	Cys	Tyr	Ser	Cys	Thr
625					630					635					640
Ala	Asn	Thr	Asn	Asp	Cys	His	Trp	Cys	Asn	Asp	His	Cys	Val	Pro	Arg
				645					650					655	
Asn	His	Ser	Cys	Ser	Glu	Gly	Gln	Ile	Ser	Ile	Phe	Arg	Tyr	Glu	Asn
			660					665					670		
Cys	Pro	Lys	Asp	Asn	Pro	Met	Tyr	Cys	Asn	Lys	Lys	Thr	Ser	Cys	
		675					680				685				
Arg	Ser	Cys	Ala	Leu	Asp	Gln	Asn	Cys	Gln	Trp	Glu	Pro	Arg	Asn	Gln
	690					695					700				
Glu	Cys	Ile	Ala	Leu	Pro	Glu	Asn	Ile	Cys	Gly	Ile	Gly	Trp	His	Leu
705					710					715					720
Val	Gly	Asn	Ser	Cys	Leu	Lys	Ile	Thr	Thr	Ala	Lys	Glu	Asn	Tyr	Asp
				725					730					735	
Asn	Ala	Lys	Leu	Phe	Cys	Arg	Asn	His	Asn	Ala	Leu	Leu	Ala	Ser	Leu
			740					745					750		
Thr	Thr	Gln	Lys	Lys	Val	Glu	Phe	Val	Leu	Lys	Gln	Leu	Arg	Ile	Met
		755					760					765			
Gln	Ser	Ser	Gln	Ser	Met	Ser	Lys	Leu	Thr	Leu	Thr	Pro	Trp	Val	Gly
	770					775					780				
Leu	Arg	Lys	Ile	Asn	Val	Ser	Tyr	Trp	Cys	Trp	Glu	Asp	Met	Ser	Pro
785					790					795					800
Phe	Thr	Asn	Ser	Leu	Leu	Gln	Trp	Met	Pro	Ser	Glu	Pro	Ser	Asp	Ala
				805					810					815	
Gly	Phe	Cys	Gly	Ile	Leu	Ser	Glu	Pro	Ser	Thr	Arg	Gly	Leu	Lys	Ala
			820					825				830			
Ala	Thr	Cys	Ile	Asn	Pro	Leu	Asn	Gly	Ser	Val	Cys	Glu	Arg	Pro	Ala
		835					840					845			
Asn	His	Ser	Ala	Lys	Gln	Cys	Arg	Thr	Pro	Cys	Ala	Leu	Arg	Thr	Ala
	850					855					860				
Cys	Gly	Asp	Cys	Thr	Ser	Gly	Ser	Ser	Glu	Cys	Met	Trp	Cys	Ser	Asn
865					870					875					880
Met	Lys	Gln	Cys	Val	Asp	Ser	Asn	Ala	Tyr	Val	Ala	Ser	Phe	Pro	Phe
				885					890					895	
Gly	Gln	Cys	Met	Glu	Trp	Tyr	Thr	Met	Ser	Thr	Cys	Pro	Pro	Glu	Asn
			900					905					910		
Cys	Ser	Gly	Tyr	Cys	Thr	Cys	Ser	His	Cys	Leu	Glu	Gln	Pro	Gly	Cys

915 920 925
 Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu
 930 935 940
 Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly
 945 950 955 960
 Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp
 965 970 975
 Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn
 980 985 990
 Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn
 995 1000 1005
 Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly
 1010 1015 1020
 Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His
 1025 1030 1035 1040
 Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys
 1045 1050 1055
 Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr
 1060 1065 1070
 Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp
 1075 1080 1085
 Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr
 1090 1095 1100
 Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp
 1105 1110 1115 1120
 Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala
 1125 1130 1135
 Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val
 1140 1145 1150
 Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys
 1155 1160 1165
 Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser
 1170 1175 1180
 Asn Phe Thr Trp Pro Ile Lys Ile Gln Val Gln Thr Glu Gln
 1185 1190 1195

<210> 3
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 3
 cccaagcttg ggatgggtgt cgggctcagc ccgc

34

<210> 4
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 4
 ataagaatgc ggcgctaaac tcattgttca gtttcgacct g

41

<210> 5
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 5
 cccaagcttg ggatggtggc cgcagcggcg gc 32

<210> 6
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 6
 ccaggtccat ctgtcacaaa cccag 25

<210> 7
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 7
 gtgcgtgaag cttgtaccgg caactgaggc aaggctga 38

<210> 8
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<400> 8
 gtagttttaa gtccacgttt gacttcgccg gcgtgcgtg 39

<210> 9
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated polypeptide

<400> 9
 Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala
 1 5 10 15

<210> 10
 <211> 1355
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr
 1 5 10 15
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val
 20 25 30
 Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala
 35 40 45
 Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu
 50 55 60
 Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr
 65 70 75 80
 Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met
 85 90 95
 Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu
 100 105 110
 Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe
 115 120 125
 Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu
 130 135 140
 Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala
 145 150 155 160
 Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys
 165 170 175
 Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser
 180 185 190
 Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys
 195 200 205
 Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile
 210 215 220
 Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln
 225 230 235 240
 Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr
 245 250 255
 Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala
 260 265 270
 Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn
 275 280 285
 His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu
 290 295 300
 Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly
 305 310 315 320
 His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys
 325 330 335
 Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile
 340 345 350
 His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr
 355 360 365
 Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg
 370 375 380
 Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile
 385 390 395 400
 Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu

													405			410			415			
His	Thr	Gln	Gly	Ala	Leu	Val	Gln	Gly	Gly	Tyr	Gly	His	Ser	Ser	Val							
													420			425			430			
Tyr	Asp	His	Arg	Thr	Arg	Ala	Leu	Tyr	Val	His	Gly	Gly	Tyr	Lys	Ala							
													435			440			445			
Phe	Ser	Ala	Asn	Lys	Tyr	Arg	Leu	Ala	Asp	Asp	Leu	Tyr	Arg	Tyr	Asp							
													450			455			460			
Val	Asp	Thr	Gln	Met	Trp	Thr	Ile	Leu	Lys	Asp	Ser	Arg	Phe	Phe	Arg							
465														470			475			480		
Tyr	Leu	His	Thr	Ala	Val	Ile	Val	Ser	Gly	Thr	Met	Leu	Val	Phe	Gly							
													485			490			495			
Gly	Asn	Thr	His	Asn	Asp	Thr	Ser	Met	Ser	His	Gly	Ala	Lys	Cys	Phe							
													500			505			510			
Ser	Ser	Asp	Phe	Met	Ala	Tyr	Asp	Ile	Ala	Cys	Asp	Arg	Trp	Ser	Val							
													515			520			525			
Leu	Pro	Arg	Pro	Asp	Leu	His	His	Asp	Val	Asn	Arg	Phe	Gly	His	Ser							
													530			535			540			
Ala	Val	Leu	His	Asn	Ser	Thr	Met	Tyr	Val	Phe	Gly	Gly	Phe	Asn	Ser							
545														550			555			560		
Leu	Leu	Leu	Ser	Asp	Ile	Leu	Val	Phe	Thr	Ser	Glu	Gln	Cys	Asp	Ala							
													565			570			575			
His	Arg	Ser	Glu	Ala	Ala	Cys	Leu	Ala	Ala	Gly	Pro	Gly	Ile	Arg	Cys							
													580			585			590			
Val	Trp	Asn	Thr	Gly	Ser	Ser	Gln	Cys	Ile	Ser	Trp	Ala	Leu	Ala	Thr							
													595			600			605			
Asp	Glu	Gln	Glu	Glu	Lys	Leu	Lys	Ser	Glu	Cys	Phe	Ser	Lys	Arg	Thr							
													610			615			620			
Leu	Asp	His	Asp	Arg	Cys	Asp	Gln	His	Thr	Asp	Cys	Tyr	Ser	Cys	Thr							
625														630			635			640		
Ala	Asn	Thr	Asn	Asp	Cys	His	Trp	Cys	Asn	Asp	His	Cys	Val	Pro	Arg							
													645			650			655			
Asn	His	Ser	Cys	Ser	Glu	Gly	Gln	Ile	Ser	Ile	Phe	Arg	Tyr	Glu	Asn							
													660			665			670			
Cys	Pro	Lys	Asp	Asn	Pro	Met	Tyr	Tyr	Cys	Asn	Lys	Lys	Thr	Ser	Cys							
													675			680			685			
Arg	Ser	Cys	Ala	Leu	Asp	Gln	Asn	Cys	Gln	Trp	Glu	Pro	Arg	Asn	Gln							
													690			695			700			
Glu	Cys	Ile	Ala	Leu	Pro	Glu	Asn	Ile	Cys	Gly	Ile	Gly	Trp	His	Leu							
705														710			715			720		
Val	Gly	Asn	Ser	Cys	Leu	Lys	Ile	Thr	Thr	Ala	Lys	Glu	Asn	Tyr	Asp							
													725			730			735			
Asn	Ala	Lys	Leu	Phe	Cys	Arg	Asn	His	Asn	Ala	Leu	Leu	Ala	Ser	Leu							
													740			745			750			
Thr	Thr	Gln	Lys	Lys	Val	Glu	Phe	Val	Leu	Lys	Gln	Leu	Arg	Ile	Met							
													755			760			765			
Gln	Ser	Ser	Gln	Ser	Met	Ser	Lys	Leu	Thr	Leu	Thr	Pro	Trp	Val	Gly							
													770			775			780			
Leu	Arg	Lys	Ile	Asn	Val	Ser	Tyr	Trp	Cys	Trp	Glu	Asp	Met	Ser	Pro							
785														790			795			800		
Phe	Thr	Asn	Ser	Leu	Leu	Gln	Trp	Met	Pro	Ser	Glu	Pro	Ser	Asp	Ala							
													805			810			815			
Gly	Phe	Cys	Gly	Ile	Leu	Ser	Glu	Pro	Ser	Thr	Arg	Gly	Leu	Lys	Ala							
													820			825			830			
Ala	Thr</																					

Cys	Gly	Asp	Cys	Thr	Ser	Gly	Ser	Ser	Glu	Cys	Met	Trp	Cys	Ser	Asn	865	870	875	880
Met	Lys	Gln	Cys	Val	Asp	Ser	Asn	Ala	Tyr	Val	Ala	Ser	Phe	Pro	Phe	885	890		895
Gly	Gln	Cys	Met	Glu	Trp	Tyr	Thr	Met	Ser	Thr	Cys	Pro	Pro	Glu	Asn	900	905		910
Cys	Ser	Gly	Tyr	Cys	Thr	Cys	Ser	His	Cys	Leu	Glu	Gln	Pro	Gly	Cys	915	920		925
Gly	Trp	Cys	Thr	Asp	Pro	Ser	Asn	Thr	Gly	Lys	Gly	Lys	Cys	Ile	Glu	930	935		940
Gly	Ser	Tyr	Lys	Gly	Pro	Val	Lys	Met	Pro	Ser	Gln	Ala	Pro	Thr	Gly	945	950		955
Asn	Phe	Tyr	Pro	Gln	Pro	Leu	Leu	Asn	Ser	Ser	Met	Cys	Leu	Glu	Asp	965	970		975
Ser	Arg	Tyr	Asn	Trp	Ser	Phe	Ile	His	Cys	Pro	Ala	Cys	Gln	Cys	Asn	980	985		990
Gly	His	Ser	Lys	Cys	Ile	Asn	Gln	Ser	Ile	Cys	Glu	Lys	Cys	Glu	Asn	995	1000		1005
Leu	Thr	Thr	Gly	Lys	His	Cys	Glu	Thr	Cys	Ile	Ser	Gly	Phe	Tyr	Gly	1010	1015		1020
Asp	Pro	Thr	Asn	Gly	Gly	Lys	Cys	Gln	Pro	Cys	Lys	Cys	Asn	Gly	His	1025	1030		1035
Ala	Ser	Leu	Cys	Asn	Thr	Asn	Thr	Gly	Lys	Cys	Phe	Cys	Thr	Thr	Lys	1045	1050		1055
Gly	Val	Lys	Gly	Asp	Glu	Cys	Gln	Leu	Cys	Glu	Val	Glu	Asn	Arg	Tyr	1060	1065		1070
Gln	Gly	Asn	Pro	Leu	Arg	Gly	Thr	Cys	Tyr	Tyr	Thr	Leu	Leu	Ile	Asp	1075	1080		1085
Tyr	Gln	Phe	Thr	Phe	Ser	Leu	Ser	Gln	Glu	Asp	Asp	Arg	Tyr	Tyr	Thr	1090	1095		1100
Ala	Ile	Asn	Phe	Val	Ala	Thr	Pro	Asp	Glu	Gln	Asn	Arg	Asp	Leu	Asp	1105	1110		1115
Met	Phe	Ile	Asn	Ala	Ser	Lys	Asn	Phe	Asn	Leu	Asn	Ile	Thr	Trp	Ala	1125	1130		1135
Ala	Ser	Phe	Ser	Ala	Gly	Thr	Gln	Ala	Gly	Glu	Glu	Met	Pro	Val	Val	1140	1145		1150
Ser	Lys	Thr	Asn	Ile	Lys	Glu	Tyr	Lys	Asp	Ser	Phe	Ser	Asn	Glu	Lys	1155	1160		1165
Phe	Asp	Phe	Arg	Asn	His	Pro	Asn	Ile	Thr	Phe	Phe	Val	Tyr	Val	Ser	1170	1175		1180
Asn	Phe	Thr	Trp	Pro	Ile	Lys	Ile	Gln	Ile	Ala	Phe	Ser	Gln	His	Ser	1185	1190		1195
Asn	Phe	Met	Asp	Leu	Val	Gln	Phe	Phe	Val	Thr	Phe	Phe	Ser	Cys	Phe	1205	1210		1215
Leu	Ser	Leu	Leu	Leu	Val	Ala	Ala	Val	Val	Trp	Lys	Ile	Lys	Gln	Ser	1220	1225		1230
Cys	Trp	Ala	Ser	Arg	Arg	Arg	Glu	Gln	Leu	Leu	Arg	Glu	Met	Gln	Gln	1235	1240		1245
Met	Ala	Ser	Arg	Pro	Phe	Ala	Ser	Val	Asn	Val	Ala	Leu	Glu	Thr	Asp	1250	1255		1260
Glu	Glu	Pro	Pro	Asp	Leu	Ile	Gly	Gly	Ser	Ile	Lys	Thr	Val	Pro	Lys	1265	1270		1275
Pro	Ile	Ala	Leu	Glu	Pro	Cys	Phe	Gly	Asn	Lys	Ala	Ala	Val	Leu	Ser	1285	1290		1295
Val	Phe	Val	Arg	Leu	Pro	Arg	Gly	Leu	Gly	Gly	Ile	Pro	Pro	Pro	Gly	1300	1305		1310
Gln	Ser	Gly	Leu	Ala	Val	Ala	Ser	Ala	Leu	Val	Asp	Ile	Ser	Gln	Gln				

1315 1320 1325
 Met Pro Ile Val Tyr Lys Glu Lys Ser Gly Ala Val Arg Asn Arg Lys
 1330 1335 1340
 Gln Gln Pro Pro Ala Gln Pro Gly Thr Cys Ile
 1345 1350 1355

<210> 11
 <211> 4068
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(4065)

<400> 11
 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48
 Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr
 1 5 10 15

 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgt gtc 96
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys Val
 20 25 30

 aac ggc ggt cgc tgc aac cct ggc acc ggc cag tgc gtc tgc ccc gcc 144
 Asn Gly Gly Arg Cys Asn Pro Gly Thr Gly Gln Cys Val Cys Pro Ala
 35 40 45

 ggc tgg gtg ggc gag caa tgc cag cac tgc ggg ggc cgc ttc aga cta 192
 Gly Trp Val Gly Glu Gln Cys Gln His Cys Gly Gly Arg Phe Arg Leu
 50 55 60

 act gga tct tct ggg ttt gtg aca gat gga cct gga aat tat aaa tac 240
 Thr Gly Ser Ser Gly Phe Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr
 65 70 75 80

 aaa acg aag tgc acg tgg ctc att gaa gga cag cca aat aga ata atg 288
 Lys Thr Lys Cys Thr Trp Leu Ile Glu Gly Gln Pro Asn Arg Ile Met
 85 90 95

 aga ctt cgt ttc aat cat ttt gct aca gag tgt agt tgg gac cat tta 336
 Arg Leu Arg Phe Asn His Phe Ala Thr Glu Cys Ser Trp Asp His Leu
 100 105 110

 tat gtt tat gat ggg gac tca att tat gca ccg cta gtt gct gca ttt 384
 Tyr Val Tyr Asp Gly Asp Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe
 115 120 125

 agt ggc ctc att gtt cct gag aga gat ggc aat gag act gtc cct gag 432
 Ser Gly Leu Ile Val Pro Glu Arg Asp Gly Asn Glu Thr Val Pro Glu
 130 135 140

 gtt gtt gcc aca tca ggt tat gcc ttg ctg cat ttt ttt agt gat gct 480
 Val Val Ala Thr Ser Gly Tyr Ala Leu Leu His Phe Phe Ser Asp Ala
 145 150 155 160

 gct tat aat ttg act gga ttt aat att act tac agt ttt gat atg tgt 528

Ala Tyr Asn Leu Thr Gly Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys	
165	170 175
cca aat aac tgc tca ggc cga gga gag tgt aag atc agt aat agc agc	576
Pro Asn Asn Cys Ser Gly Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser	
180	185 190
gat act gtt gaa tgt gaa tgt tct gaa aac tgg aaa ggt gaa gca tgt	624
Asp Thr Val Glu Cys Glu Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys	
195	200 205
gac att cct cac tgt aca gac aac tgt ggt ttt cct cat cga ggc atc	672
Asp Ile Pro His Cys Thr Asp Asn Cys Gly Phe Pro His Arg Gly Ile	
210	215 220
tgc aat tca agt gat gtc aga gga tgc tcc tgc ttc tca gac tgg cag	720
Cys Asn Ser Ser Asp Val Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln	
225	230 235 240
ggg cct gga tgt tca gtt cct gta cca gct aac cag tca ttt tgg act	768
Gly Pro Gly Cys Ser Val Pro Val Pro Ala Asn Gln Ser Phe Trp Thr	
245	250 255
cga gag gaa tat tct aac tta aag ctc ccc aga gca tct cat aaa gct	816
Arg Glu Glu Tyr Ser Asn Leu Lys Leu Pro Arg Ala Ser His Lys Ala	
260	265 270
gtg gtc aat gga aac att atg tgg gtt gtt gga gga tat atg ttc aac	864
Val Val Asn Gly Asn Ile Met Trp Val Val Gly Gly Tyr Met Phe Asn	
275	280 285
cac tca gat tat aac atg gtt cta gcg tat gac ctt gct tct agg gag	912
His Ser Asp Tyr Asn Met Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu	
290	295 300
tgg ctt cca cta aac cgt tct gtg aac aat gtg gtt gtt aga tat ggt	960
Trp Leu Pro Leu Asn Arg Ser Val Asn Asn Val Val Val Arg Tyr Gly	
305	310 315 320
cat tct ttg gca tta tac aag gat aaa att tac atg tat gga gga aaa	1008
His Ser Leu Ala Leu Tyr Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys	
325	330 335
att gat tca act ggg aat gtg acc aat gag ttg aga gtt ttt cac att	1056
Ile Asp Ser Thr Gly Asn Val Thr Asn Glu Leu Arg Val Phe His Ile	
340	345 350
cat aat gag tca tgg gtg ttg ttg acc cct aag gca aag gag cag tat	1104
His Asn Glu Ser Trp Val Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr	
355	360 365
gca gtg gtt ggg cac tct gca cac att gtt aca ctg aag aat ggc cga	1152
Ala Val Val Gly His Ser Ala His Ile Val Thr Leu Lys Asn Gly Arg	
370	375 380
gtg gtc atg ctg gtc atc ttt ggt cac tgc cct ctc tat gga tat ata	1200
Val Val Met Leu Val Ile Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile	

385	390	395	400	
agc aat gtg cag gaa tat gat ttg gat aag aac aca tgg agt ata tta				1248
Ser Asn Val Gln Glu Tyr Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu				
	405	410	415	
cac acc cag ggt gcc ctt gtg caa ggg ggt tac ggc cat agc agt gtt				1296
His Thr Gln Gly Ala Leu Val Gln Gly Tyr Gly His Ser Ser Val				
	420	425	430	
tac gac cat agg acc agg gcc cta tac gtt cat ggt ggc tac aag gct				1344
Tyr Asp His Arg Thr Arg Ala Leu Tyr Val His Gly Gly Tyr Lys Ala				
	435	440	445	
ttc agt gcc aat aag tac cgg ctt gca gat gat ctc tac cga tat gat				1392
Phe Ser Ala Asn Lys Tyr Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp				
	450	455	460	
gtg gat acc cag atg tgg acc att ctt aag gac agc cga ttt ttc cgt				1440
Val Asp Thr Gln Met Trp Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg				
	465	470	475	480
tac ttg cac aca gct gtg ata gtg agt gga acc atg ctg gtg ttt ggg				1488
Tyr Leu His Thr Ala Val Ile Val Ser Gly Thr Met Leu Val Phe Gly				
	485	490	495	
gga aac aca cac aat gac aca tct atg agc cat ggc gcc aaa tgc ttc				1536
Gly Asn Thr His Asn Asp Thr Ser Met Ser His Gly Ala Lys Cys Phe				
	500	505	510	
tct tca gat ttc atg gcc tat gac att gcc tgt gac cgc tgg tca gtg				1584
Ser Ser Asp Phe Met Ala Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val				
	515	520	525	
ctt ccc aga cct gat ctc cac cat gat gtc aac aga ttt ggc cat tca				1632
Leu Pro Arg Pro Asp Leu His His Asp Val Asn Arg Phe Gly His Ser				
	530	535	540	
gca gtc tta cac aac agc acc atg tat gtg ttc ggt ggt ttc aat agt				1680
Ala Val Leu His Asn Ser Thr Met Tyr Val Phe Gly Gly Phe Asn Ser				
	545	550	555	560
ctc ctc ctc agc gac atc ctg gta ttc acc tcg gaa cag tgt gat gcg				1728
Leu Leu Leu Ser Asp Ile Leu Val Phe Thr Ser Glu Gln Cys Asp Ala				
	565	570	575	
cat cgg agt gaa gcc gct tgt tta gca gca gga cct ggt att cgg tgt				1776
His Arg Ser Glu Ala Ala Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys				
	580	585	590	
gtg tgg aac aca ggg tcg tct cag tgt atc tcg tgg gcg ctg gca act				1824
Val Trp Asn Thr Gly Ser Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr				
	595	600	605	
gat gaa caa gaa gaa aag tta aaa tca gaa tgt ttt tcc aaa aga act				1872
Asp Glu Gln Glu Glu Lys Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr				
	610	615	620	

ctt gac cat gac aga tgt gac cag cac aca gat tgt tac agc tgc aca Leu Asp His Asp Arg Cys Asp Gln His Thr Asp Cys Tyr Ser Cys Thr 625 630 635 640	1920
gcc aac acc aat gac tgc cac tgg tgc aat gac cat tgt gtc ccc agg Ala Asn Thr Asn Asp Cys His Trp Cys Asn Asp His Cys Val Pro Arg 645 650 655	1968
aac cac agc tgc tca gaa ggc cag atc tcc att ttt agg tat gag aat Asn His Ser Cys Ser Glu Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn 660 665 670	2016
tgc ccc aag gat aac cct atg tac tac tgt aac aag aag acc agc tgc Cys Pro Lys Asp Asn Pro Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys 675 680 685	2064
agg agc tgt gcc ctg gac cag aac tgc cag tgg gag ccc cgg aat cag Arg Ser Cys Ala Leu Asp Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln 690 695 700	2112
gag tgc att gcc ctg ccc gaa aat atc tgt ggc att ggc tgg cat ttg Glu Cys Ile Ala Leu Pro Glu Asn Ile Cys Gly Ile Gly Trp His Leu 705 710 715 720	2160
gtt gga aac tca tgt ttg aaa att act act gcc aag gag aat tat gac Val Gly Asn Ser Cys Leu Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp 725 730 735	2208
aat gct aaa ttg ttc tgt agg aac cac aat gcc ctt ttg gct tct ctt Asn Ala Lys Leu Phe Cys Arg Asn His Asn Ala Leu Leu Ala Ser Leu 740 745 750	2256
aca acc cag aag aag gta gaa ttt gtc ctt aag cag ctg cga ata atg Thr Thr Gln Lys Lys Val Glu Phe Val Leu Lys Gln Leu Arg Ile Met 755 760 765	2304
cag tca tct cag agc atg tcc aag ctc acc tta acc cca tgg gtc ggc Gln Ser Ser Gln Ser Met Ser Lys Leu Thr Leu Thr Pro Trp Val Gly 770 775 780	2352
ctt cgg aag atc aat gtg tcc tac tgg tgc tgg gaa gat atg tcc cca Leu Arg Lys Ile Asn Val Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro 785 790 795 800	2400
ttt aca aat agt tta cta cag tgg atg ccg tct gag ccc agt gat gct Phe Thr Asn Ser Leu Leu Gln Trp Met Pro Ser Glu Pro Ser Asp Ala 805 810 815	2448
gga ttc tgt gga att tta tca gaa ccc agt act cgg gga ctg aag gct Gly Phe Cys Gly Ile Leu Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala 820 825 830	2496
gca acc tgc atc aac cca ctc aat ggt agt gtc tgt gaa agg cct gca Ala Thr Cys Ile Asn Pro Leu Asn Gly Ser Val Cys Glu Arg Pro Ala 835 840 845	2544

aac cac agt gct aag cag tgc cgg aca cca tgt gcc ttg agg aca gca Asn His Ser Ala Lys Gln Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala 850 855 860	2592
tgt gga gat tgc acc agc ggc agc tct gag tgc atg tgg tgc agc aac Cys Gly Asp Cys Thr Ser Gly Ser Ser Glu Cys Met Trp Cys Ser Asn 865 870 875 880	2640
atg aag cag tgt gtg gac tcc aat gcc tat gtg gcc tcc ttc cct ttt Met Lys Gln Cys Val Asp Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe 885 890 895	2688
ggc cag tgt atg gaa tgg tat acg atg agc acc tgc ccc cct gaa aat Gly Gln Cys Met Glu Trp Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn 900 905 910	2736
tgt tca ggc tac tgt acc tgt agt cat tgc ttg gag caa cca ggc tgt Cys Ser Gly Tyr Cys Thr Cys Ser His Cys Leu Glu Gln Pro Gly Cys 915 920 925	2784
ggc tgg tgt act gat ccc agc aat act ggc aaa ggg aaa tgc ata gag Gly Trp Cys Thr Asp Pro Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu 930 935 940	2832
ggc tcc tat aaa gga cca gtg aag atg cct tcg caa gcc cct aca gga Gly Ser Tyr Lys Gly Pro Val Lys Met Pro Ser Gln Ala Pro Thr Gly 945 950 955 960	2880
aat ttc tat cca cag ccc ctg ctc aat tcc agc atg tgt cta gag gac Asn Phe Tyr Pro Gln Pro Leu Leu Asn Ser Ser Met Cys Leu Glu Asp 965 970 975	2928
agc aga tac aac tgg tct ttc att cac tgt cca gct tgc caa tgc aac Ser Arg Tyr Asn Trp Ser Phe Ile His Cys Pro Ala Cys Gln Cys Asn 980 985 990	2976
ggc cac agt aaa tgc atc aat cag agc atc tgt gag aag tgt gag aac Gly His Ser Lys Cys Ile Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn 995 1000 1005	3024
ctg acc aca ggc aag cac tgc gag acc tgc ata tct ggc ttc tac ggt Leu Thr Thr Gly Lys His Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly 1010 1015 1020	3072
gat ccc acc aat gga ggg aaa tgt cag cca tgc aag tgc aat ggg cac Asp Pro Thr Asn Gly Gly Lys Cys Gln Pro Cys Lys Cys Asn Gly His 1025 1030 1035 1040	3120
gcg tct ctg tgc aac acc aac acg ggc aag tgc ttc tgc acc acc aag Ala Ser Leu Cys Asn Thr Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys 1045 1050 1055	3168
ggc gtc aag ggg gac gag tgc cag cta tgt gag gta gaa aat cga tac Gly Val Lys Gly Asp Glu Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr 1060 1065 1070	3216
caa gga aac cct ctc aga gga aca tgt tat tat act ctt ctt att gac	3264

Gln Gly Asn Pro Leu Arg Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp	
1075	1080 1085
tat cag ttc acc ttt agt cta tcc cag gaa gat gat cgc tat tac aca	3312
Tyr Gln Phe Thr Phe Ser Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr	
1090	1095 1100
gct atc aat ttt gtg gct act cct gac gaa caa aac agg gat ttg gac	3360
Ala Ile Asn Phe Val Ala Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp	
1105	1110 1115 1120
atg ttc atc aat gcc tcc aag aat ttc aac ctc aac atc acc tgg gct	3408
Met Phe Ile Asn Ala Ser Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala	
	1125 1130 1135
gcc agt ttc tca gct gga acc cag gct gga gaa gag atg cct gtt gtt	3456
Ala Ser Phe Ser Ala Gly Thr Gln Ala Gly Glu Glu Met Pro Val Val	
	1140 1145 1150
tca aaa acc aac att aag gag tac aaa gat agt ttc tct aat gag aag	3504
Ser Lys Thr Asn Ile Lys Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys	
	1155 1160 1165
ttt gat ttt cgc aac cac cca aat atc act ttc ttt gtt tat gtc agt	3552
Phe Asp Phe Arg Asn His Pro Asn Ile Thr Phe Phe Val Tyr Val Ser	
	1170 1175 1180
aat ttc acc tgg ccc atc aaa att cag att gcc ttc tct cag cac agc	3600
Asn Phe Thr Trp Pro Ile Lys Ile Gln Ile Ala Phe Ser Gln His Ser	
	1185 1190 1195 1200
aat ttt atg gac ctg gta cag ttc ttc gtg act ttc ttc agt tgt ttc	3648
Asn Phe Met Asp Leu Val Gln Phe Phe Val Thr Phe Phe Ser Cys Phe	
	1205 1210 1215
ctc tct ttg ctc ctg gtg gct gct gtg gtt tgg aag atc aaa caa agt	3696
Leu Ser Leu Leu Leu Val Ala Ala Val Val Trp Lys Ile Lys Gln Ser	
	1220 1225 1230
tgt tgg gcc tcc aga cgt aga gag caa ctt ctt cga gag atg caa cag	3744
Cys Trp Ala Ser Arg Arg Arg Glu Gln Leu Leu Arg Glu Met Gln Gln	
	1235 1240 1245
atg gcc agc cgt ccc ttt gcc tct gta aat gtc gcc ttg gaa aca gat	3792
Met Ala Ser Arg Pro Phe Ala Ser Val Asn Val Ala Leu Glu Thr Asp	
	1250 1255 1260
gag gag cct cct gat ctt att ggg ggg agt ata aag act gtt ccc aaa	3840
Glu Glu Pro Pro Asp Leu Ile Gly Gly Ser Ile Lys Thr Val Pro Lys	
	1265 1270 1275 1280
ccc att gca ctg gag ccg tgt ttt ggc aac aaa gcc gct gtc ctc tct	3888
Pro Ile Ala Leu Glu Pro Cys Phe Gly Asn Lys Ala Ala Val Leu Ser	
	1285 1290 1295
gtg ttt gtg agg ctc cct cga ggc ctg ggt ggc atc cct cct cct ggg	3936
Val Phe Val Arg Leu Pro Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly	

1300	1305	1310	
cag tca ggt ctt gct gtg gcc agc gcc ctg gtg gac att tct cag cag			3984
Gln Ser Gly Leu Ala Val Ala Ser Ala Leu Val Asp Ile Ser Gln Gln			
1315	1320	1325	
atg ccg ata gtg tac aag gag aag tca gga gcc gtg aga aac cgg aag			4032
Met Pro Ile Val Tyr Lys Glu Lys Ser Gly Ala Val Arg Asn Arg Lys			
1330	1335	1340	
cag cag ccc cct gca cag cct ggg acc tgc atc tga			4068
Gln Gln Pro Pro Ala Gln Pro Gly Thr Cys Ile			
1345	1350	1355	

<210> 12
 <211> 1429
 <212> PRT
 <213> Homo sapiens

<400> 12

Met	Val	Ala	Ala	Ala	Ala	Ala	Thr	Glu	Ala	Arg	Leu	Arg	Arg	Arg	Thr
1				5					10					15	
Ala	Ala	Thr	Ala	Ala	Leu	Ala	Gly	Arg	Ser	Gly	Gly	Pro	His	Trp	Asp
			20					25					30		
Trp	Asp	Val	Thr	Arg	Ala	Gly	Arg	Pro	Gly	Leu	Gly	Ala	Gly	Leu	Arg
	35						40					45			
Leu	Pro	Arg	Leu	Leu	Ser	Pro	Pro	Leu	Arg	Pro	Arg	Leu	Leu	Leu	Leu
	50					55					60				
Leu	Leu	Leu	Leu	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Cys	Glu
	65				70				75					80	
Ala	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Val	Ser	Gly	Ser	Ala	Ala	Ala
				85					90					95	
Glu	Ala	Lys	Glu	Cys	Asp	Arg	Pro	Cys	Val	Asn	Gly	Gly	Arg	Cys	Asn
			100					105					110		
Pro	Gly	Thr	Gly	Gln	Cys	Val	Cys	Pro	Ala	Gly	Trp	Val	Gly	Glu	Gln
		115					120					125			
Cys	Gln	His	Cys	Gly	Gly	Arg	Phe	Arg	Leu	Thr	Gly	Ser	Ser	Gly	Phe
	130					135					140				
Val	Thr	Asp	Gly	Pro	Gly	Asn	Tyr	Lys	Tyr	Lys	Thr	Lys	Cys	Thr	Trp
	145				150				155					160	
Leu	Ile	Glu	Gly	Gln	Pro	Asn	Arg	Ile	Met	Arg	Leu	Arg	Phe	Asn	His
				165				170						175	
Phe	Ala	Thr	Glu	Cys	Ser	Trp	Asp	His	Leu	Tyr	Val	Tyr	Asp	Gly	Asp
			180					185					190		
Ser	Ile	Tyr	Ala	Pro	Leu	Val	Ala	Ala	Phe	Ser	Gly	Leu	Ile	Val	Pro
		195					200					205			
Glu	Arg	Asp	Gly	Asn	Glu	Thr	Val	Pro	Glu	Val	Val	Ala	Thr	Ser	Gly
	210					215					220				
Tyr	Ala	Leu	Leu	His	Phe	Phe	Ser	Asp	Ala	Ala	Tyr	Asn	Leu	Thr	Gly
	225				230				235					240	
Phe	Asn	Ile	Thr	Tyr	Ser	Phe	Asp	Met	Cys	Pro	Asn	Asn	Cys	Ser	Gly
				245				250					255		
Arg	Gly	Glu	Cys	Lys	Ile	Ser	Asn	Ser	Ser	Glu	Thr	Val	Glu	Cys	Glu
			260				265					270			
Cys	Ser	Glu	Asn	Trp	Lys	Gly	Glu	Ala	Cys	Asp	Ile	Pro	His	Cys	Thr
	275					280						285			
Asp	Asn	Cys	Gly	Phe	Pro	His	Arg	Gly	Ile	Cys	Asn	Ser	Ser	Asp	Val

290	295	300
Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val		
305	310	315
Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn		
	325	330
Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile		
	340	345
Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met		
	355	360
Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg		
	370	375
Ser Val Asn Asn Val Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr		
385	390	395
Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn		
	405	410
Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val		
	420	425
Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser		
	435	440
Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile		
	450	455
Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr		
465	470	475
Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu		
	485	490
Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg		
	500	505
Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr		
	515	520
Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp		
	530	535
Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val		
545	550	555
Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp		
	565	570
Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala		
	580	585
Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu		
	595	600
His His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser		
	610	615
Thr Met Tyr Val Phe Gly Gly Phe Asn Ser Leu Leu Leu Ser Asp Ile		
625	630	635
Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala		
	645	650
Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser		
	660	665
Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Glu Lys		
	675	680
Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys		
	690	695
Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys		
705	710	715
His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu		
	725	730
Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro		
	740	745
		750

Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp
 755 760 765
 Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro
 770 775 780
 Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu
 785 790 795 800
 Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys
 805 810 815
 Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val
 820 825 830
 Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met
 835 840 845
 Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val
 850 855 860
 Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu
 865 870 875 880
 Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu
 885 890 895
 Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro
 900 905 910
 Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln
 915 920 925
 Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser
 930 935 940
 Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp
 945 950 955 960
 Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp
 965 970 975
 Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr
 980 985 990
 Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro
 995 1000 1005
 Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro
 1010 1015 1020
 Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro
 1025 1030 1035 1040
 Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser
 1045 1050 1055
 Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile
 1060 1065 1070
 Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His
 1075 1080 1085
 Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly
 1090 1095 1100
 Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr
 1105 1110 1115 1120
 Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu
 1125 1130 1135
 Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg
 1140 1145 1150
 Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser
 1155 1160 1165
 Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala
 1170 1175 1180
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser
 1185 1190 1195 1200
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly

1205 1210 1215
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys
 1220 1225 1230
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His
 1235 1240 1245
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile
 1250 1255 1260
 Lys Ile Gln Ile Ala Phe Ser Gln His Ser Asn Phe Met Asp Leu Val
 1265 1270 1275 1280
 Gln Phe Phe Val Thr Phe Phe Ser Cys Phe Leu Ser Leu Leu Leu Val
 1285 1290 1295
 Ala Ala Val Val Trp Lys Ile Lys Gln Ser Cys Trp Ala Ser Arg Arg
 1300 1305 1310
 Arg Glu Gln Leu Leu Arg Glu Met Gln Gln Met Ala Ser Arg Pro Phe
 1315 1320 1325
 Ala Ser Val Asn Val Ala Leu Glu Thr Asp Glu Glu Pro Pro Asp Leu
 1330 1335 1340
 Ile Gly Gly Ser Ile Lys Thr Val Pro Lys Pro Ile Ala Leu Glu Pro
 1345 1350 1355 1360
 Cys Phe Gly Asn Lys Ala Ala Val Leu Ser Val Phe Val Arg Leu Pro
 1365 1370 1375
 Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly Gln Ser Gly Leu Ala Val
 1380 1385 1390
 Ala Ser Ala Leu Val Asp Ile Ser Gln Gln Met Pro Ile Val Tyr Lys
 1395 1400 1405
 Glu Lys Ser Gly Ala Val Arg Asn Arg Lys Gln Gln Pro Pro Ala Gln
 1410 1415 1420
 Pro Gly Thr Cys Ile
 1425

<210> 13
 <211> 4290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (4287)

<400> 13
 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48
 Met Val Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr
 1 5 10 15
 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgg gac 96
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp
 20 25 30
 tgg gac gtg acc agg gct ggg agg ccg ggg ctg ggg gcc ggg ctg cgc 144
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg
 35 40 45
 ctc ccg cgg ctg ctg tct cca ccg ctg cgg cca cgg ctg ctg ctg ctg 192
 Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu
 50 55 60
 ctg ttg ttg ctc ccg ccg ccg ctg ttg ctg ctg ctg ccc tgt gag 240

Leu	Leu	Leu	Leu	Pro	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Cys	Glu		
65						70					75				80		
gcc	gag	gcc	gcg	gcg	gcg	gcg	gcg	gcg	gtg	tcg	ggc	tca	gcc	gca	gcc		288
Ala	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Val	Ser	Gly	Ser	Ala	Ala	Ala		
				85					90					95			
gag	gcc	aag	gaa	tgt	gac	cgg	ccc	tgt	gtc	aac	ggc	ggt	cgc	tgc	aac		336
Glu	Ala	Lys		Glu	Cys	Asp	Arg	Pro	Cys	Val	Asn	Gly	Gly	Arg	Cys	Asn	
			100					105					110				
cct	ggc	acc	ggc	cag	tgc	gtc	tgc	ccc	gcc	ggc	tgg	gtg	ggc	gag	caa		384
Pro	Gly	Thr	Gly	Gln	Cys	Val	Cys	Pro	Ala	Gly	Trp	Val	Gly	Glu	Gln		
		115					120					125					
tgc	cag	cac	tgc	ggg	ggc	cgc	ttc	aga	cta	act	gga	tct	tct	ggg	ttt		432
Cys	Gln	His	Cys	Gly	Gly	Arg	Phe	Arg	Leu	Thr	Gly	Ser	Ser	Gly	Phe		
	130					135					140						
gtg	aca	gat	gga	cct	gga	aat	tat	aaa	tac	aaa	acg	aag	tgc	acg	tgg		480
Val	Thr	Asp	Gly	Pro	Gly	Asn	Tyr	Lys	Tyr	Lys	Thr	Lys	Cys	Thr	Trp		
145					150					155					160		
ctc	att	gaa	gga	cag	cca	aat	aga	ata	atg	aga	ctt	cgt	ttc	aat	cat		528
Leu	Ile	Glu	Gly	Gln	Pro	Asn	Arg	Ile	Met	Arg	Leu	Arg	Phe	Asn	His		
				165					170					175			
ttt	gct	aca	gag	tgt	agt	tgg	gac	cat	tta	tat	gtt	tat	gat	ggg	gac		576
Phe	Ala	Thr	Glu	Cys	Ser	Trp	Asp	His	Leu	Tyr	Val	Tyr	Asp	Gly	Asp		
			180					185					190				
tca	att	tat	gca	ccg	cta	gtt	gct	gca	ttt	agt	ggc	ctc	att	gtt	cct		624
Ser	Ile	Tyr	Ala	Pro	Leu	Val	Ala	Ala	Phe	Ser	Gly	Leu	Ile	Val	Pro		
		195					200					205					
gag	aga	gat	ggc	aat	gag	act	gtc	cct	gag	gtt	gtt	gcc	aca	tca	ggt		672
Glu	Arg	Asp	Gly	Asn	Glu	Thr	Val	Pro	Glu	Val	Val	Ala	Thr	Ser	Gly		
	210					215					220						
tat	gcc	ttg	ctg	cat	ttt	ttt	agt	gat	gct	gct	tat	aat	ttg	act	gga		720
Tyr	Ala	Leu	Leu	His	Phe	Phe	Ser	Asp	Ala	Ala	Tyr	Asn	Leu	Thr	Gly		
225					230					235				240			
ttt	aat	att	act	tac	agt	ttt	gat	atg	tgt	cca	aat	aac	tgc	tca	ggc		768
Phe	Asn	Ile	Thr	Tyr	Ser	Phe	Asp	Met	Cys	Pro	Asn	Asn	Cys	Ser	Gly		
			245						250				255				
cga	gga	gag	tgt	aag	atc	agt	aat	agc	agc	gaa	act	gtt	gaa	tgt	gaa		816
Arg	Gly	Glu	Cys	Lys	Ile	Ser	Asn	Ser	Ser	Glu	Thr	Val	Glu	Cys	Glu		
			260					265					270				
tgt	tct	gaa	aac	tgg	aaa	ggt	gaa	gca	tgt	gac	att	cct	cac	tgt	aca		864
Cys	Ser	Glu	Asn	Trp	Lys	Gly	Glu	Ala	Cys	Asp	Ile	Pro	His	Cys	Thr		
		275					280					285					
gac	aac	tgt	ggt	ttt	cct	cat	cga	ggc	atc	tgc	aat	tca	agt	gat	gtc		912
Asp	Asn	Cys	Gly	Phe	Pro	His	Arg	Gly	Ile	Cys	Asn	Ser	Ser	Asp	Val		

290	295	300	
aga gga tgc tcc tgc ttc tca gac tgg cag ggt cct gga tgt tca gtt			960
Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val			
305	310	315	320
cct gta cca gct aac cag tca ttt tgg act cga gag gaa tat tct aac			1008
Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn			
	325	330	335
tta aag ctc ccc aga gca tct cat aaa gct gtg gtc aat gga aac att			1056
Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile			
	340	345	350
atg tgg gtt gtt gga gga tat atg ttc aac cac tca gat tat aac atg			1104
Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met			
	355	360	365
gtt cta gcg tat gac ctt gct tct agg gag tgg ctt cca cta aac cgt			1152
Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg			
	370	375	380
tct gtg aac aat gtg gtt gtt aga tat ggt cat tct ttg gca tta tac			1200
Ser Val Asn Asn Val Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr			
	385	390	400
aag gat aaa att tac atg tat gga gga aaa att gat cca act ggg aat			1248
Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn			
	405	410	415
gtg acc aat gag ttg aga gtt ttt cac att cat aat gag tca tgg gtg			1296
Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val			
	420	425	430
ttg ttg acc cct aag gca aag gag cag tat gca gtg gtt ggg cac tct			1344
Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser			
	435	440	445
gca cac att gtt aca ctg aag aat ggc cga gtg gtc atg ctg gtc atc			1392
Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile			
	450	455	460
ttt ggt cac tgc cct ctc tat gga tat ata agc aat gtg cag gaa tat			1440
Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr			
	465	470	480
gat ttg gat aag aac aca tgg agt ata tta cac acc cag ggt gcc ctt			1488
Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu			
	485	490	495
gtg caa ggg ggt tac ggc cat agc agt gtt tac gac cat agg acc agg			1536
Val Gln Gly Gly Tyr Gly His Ser Ser Val Tyr Asp His Arg Thr Arg			
	500	505	510
gcc cta tac gtt cat ggt ggc tac aag gct ttc agt gcc aat aag tac			1584
Ala Leu Tyr Val His Gly Gly Tyr Lys Ala Phe Ser Ala Asn Lys Tyr			
	515	520	525

cgg ctt gca gat gat ctc tac cga tat gat gtg gat acc cag atg tgg Arg Leu Ala Asp Asp Leu Tyr Arg Tyr Asp Val Asp Thr Gln Met Trp 530 535 540	1632
acc att ctt aag gac agc cga ttt ttc cgt tac ttg cac aca gct gtg Thr Ile Leu Lys Asp Ser Arg Phe Phe Arg Tyr Leu His Thr Ala Val 545 550 555 560	1680
ata gtg agt gga acc atg ctg gtg ttt ggg gga aac aca cac aat gac Ile Val Ser Gly Thr Met Leu Val Phe Gly Gly Asn Thr His Asn Asp 565 570 575	1728
aca tct atg agc cat ggc gcc aaa tgc ttc tct tca gat ttc atg gcc Thr Ser Met Ser His Gly Ala Lys Cys Phe Ser Ser Asp Phe Met Ala 580 585 590	1776
tat gac att gcc tgt gac cgc tgg tca gtg ctt ccc aga cct gat ctc Tyr Asp Ile Ala Cys Asp Arg Trp Ser Val Leu Pro Arg Pro Asp Leu 595 600 605	1824
cac cat gat gtc aac aga ttt ggc cat tca gca gtc tta cac aac agc His His Asp Val Asn Arg Phe Gly His Ser Ala Val Leu His Asn Ser 610 615 620	1872
acc atg tat gtg ttc ggt ggt ttc aat agt ctc ctc ctc agc gac atc Thr Met Tyr Val Phe Gly Gly Phe Asn Ser Leu Leu Leu Ser Asp Ile 625 630 635 640	1920
ctg gta ttc acc tcg gaa cag tgt gat gcg cat cgg agt gaa gcc gct Leu Val Phe Thr Ser Glu Gln Cys Asp Ala His Arg Ser Glu Ala Ala 645 650 655	1968
tgt tta gca gca gga cct ggt att cgg tgt gtg tgg aac aca ggg tcg Cys Leu Ala Ala Gly Pro Gly Ile Arg Cys Val Trp Asn Thr Gly Ser 660 665 670	2016
tct cag tgt atc tcg tgg gcg ctg gca act gat gaa caa gaa gaa aag Ser Gln Cys Ile Ser Trp Ala Leu Ala Thr Asp Glu Gln Glu Glu Lys 675 680 685	2064
tta aaa tca gaa tgt ttt tcc aaa aga act ctt gac cat gac aga tgt Leu Lys Ser Glu Cys Phe Ser Lys Arg Thr Leu Asp His Asp Arg Cys 690 695 700	2112
gac cag cac aca gat tgt tac agc tgt aca gcc aac acc aat gac tgc Asp Gln His Thr Asp Cys Tyr Ser Cys Thr Ala Asn Thr Asn Asp Cys 705 710 715 720	2160
cac tgg tgc aat gac cat tgt gtc ccc agg aac cac agc tgc tca gaa His Trp Cys Asn Asp His Cys Val Pro Arg Asn His Ser Cys Ser Glu 725 730 735	2208
ggc cag atc tcc att ttt agg tat gag aat tgc ccc aag gat aac ccc Gly Gln Ile Ser Ile Phe Arg Tyr Glu Asn Cys Pro Lys Asp Asn Pro 740 745 750	2256

atg tac tac tgt aac aag aag acc agc tgc agg agc tgt gcc ctg gac Met Tyr Tyr Cys Asn Lys Lys Thr Ser Cys Arg Ser Cys Ala Leu Asp 755 760 765	2304
cag aac tgc cag tgg gag ccc cgg aat cag gag tgc att gcc ctg ccc Gln Asn Cys Gln Trp Glu Pro Arg Asn Gln Glu Cys Ile Ala Leu Pro 770 775 780	2352
gaa aat atc tgt ggc att ggc tgg cat ttg gtt gga aac tca tgt ttg Glu Asn Ile Cys Gly Ile Gly Trp His Leu Val Gly Asn Ser Cys Leu 785 790 795 800	2400
aaa att act act gcc aag gag aat tat gac aat gct aaa ttg ttc tgt Lys Ile Thr Thr Ala Lys Glu Asn Tyr Asp Asn Ala Lys Leu Phe Cys 805 810 815	2448
agg aac cac aat gcc ctt ttg gct tct ctt aca acc cag aag aag gta Arg Asn His Asn Ala Leu Leu Ala Ser Leu Thr Thr Gln Lys Lys Val 820 825 830	2496
gaa ttt gtc ctt aag cag ctg cga ata atg cag tca tct cag agc atg Glu Phe Val Leu Lys Gln Leu Arg Ile Met Gln Ser Ser Gln Ser Met 835 840 845	2544
tcc aag ctc acc tta acc cca tgg gtc ggc ctt cgg aag atc aat gtg Ser Lys Leu Thr Leu Thr Pro Trp Val Gly Leu Arg Lys Ile Asn Val 850 855 860	2592
tcc tac tgg tgc tgg gaa gat atg tcc cca ttt aca aat agt tta cta Ser Tyr Trp Cys Trp Glu Asp Met Ser Pro Phe Thr Asn Ser Leu Leu 865 870 875 880	2640
cag tgg atg ccg tct gag ccc agt gat gct gga ttc tgt gga att tta Gln Trp Met Pro Ser Glu Pro Ser Asp Ala Gly Phe Cys Gly Ile Leu 885 890 895	2688
tca gaa ccc agt act cgg gga ctg aag gct gca acc tgc atc aac cca Ser Glu Pro Ser Thr Arg Gly Leu Lys Ala Ala Thr Cys Ile Asn Pro 900 905 910	2736
ctc aat ggt agt gtc tgt gaa agg cct gca aac cac agt gct aag cag Leu Asn Gly Ser Val Cys Glu Arg Pro Ala Asn His Ser Ala Lys Gln 915 920 925	2784
tgc cgg aca cca tgt gcc ttg agg aca gca tgt gga gat tgc acc agc Cys Arg Thr Pro Cys Ala Leu Arg Thr Ala Cys Gly Asp Cys Thr Ser 930 935 940	2832
ggc agc tct gag tgc atg tgg tgc agc aac atg aag cag tgt gtg gac Gly Ser Ser Glu Cys Met Trp Cys Ser Asn Met Lys Gln Cys Val Asp 945 950 955 960	2880
tcc aat gcc tat gtg gcc tcc ttc cct ttt ggc cag tgt atg gaa tgg Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp 965 970 975	2928
tat acg atg agc acc tgc ccc cct gaa aat tgt tca ggc tac tgt acc	2976

Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr	
980 985 990	
tgt agt cat tgc ttg gag caa cca ggc tgt ggc tgg tgt act gat ccc	3024
Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro	
995 1000 1005	
agc aat act ggc aaa ggg aaa tgc ata gag ggt tcc tat aaa gga cca	3072
Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro	
1010 1015 1020	
gtg aag atg cct tgc caa gcc cct aca gga aat ttc tat cca cag ccc	3120
Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro	
1025 1030 1035 1040	
ctg ctc aat tcc agc atg tgt cta gag gac agc aga tac aac tgg tct	3168
Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser	
1045 1050 1055	
ttc att cac tgt cca gct tgc caa tgc aac ggc cac agt aaa tgc atc	3216
Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile	
1060 1065 1070	
aat cag agc atc tgt gag aag tgt gag aac ctg acc aca ggc aag cac	3264
Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His	
1075 1080 1085	
tgc gag acc tgc ata tct ggc ttc tac ggt gat ccc acc aat gga ggg	3312
Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly	
1090 1095 1100	
aaa tgt cag cca tgc aag tgc aat ggg cac gcg tct ctg tgc aac acc	3360
Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr	
1105 1110 1115 1120	
aac acg ggc aag tgc ttc tgc acc acc aag ggc gtc aag ggg gac gag	3408
Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu	
1125 1130 1135	
tgc cag cta tgt gag gta gaa aat cga tac caa gga aac cct ctc aga	3456
Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg	
1140 1145 1150	
gga aca tgt tat tat act ctt ctt att gac tat cag ttc acc ttt agt	3504
Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser	
1155 1160 1165	
cta tcc cag gaa gat gat cgc tat tac aca gct atc aat ttt gtg gct	3552
Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala	
1170 1175 1180	
act cct gac gaa caa aac agg gat ttg gac atg ttc atc aat gcc tcc	3600
Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser	
1185 1190 1195 1200	
aag aat ttc aac ctc aac atc acc tgg gct gcc agt ttc tca gct gga	3648
Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly	

1205	1210	1215	
acc cag gct gga gaa gag atg cct gtt gtt tca aaa acc aac att aag Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys 1220 1225 1230			3696
gag tac aaa gat agt ttc tct aat gag aag ttt gat ttt cgc aac cac Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His 1235 1240 1245			3744
cca aat atc act ttc ttt gtt tat gtc agt aat ttc acc tgg ccc atc Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile 1250 1255 1260			3792
aaa att cag att gcc ttc tct cag cac agc aat ttt atg gac ctg gta Lys Ile Gln Ile Ala Phe Ser Gln His Ser Asn Phe Met Asp Leu Val 1265 1270 1275 1280			3840
cag ttc ttc gtg act ttc ttc agt tgt ttc ctc tct ttg ctc ctg gtg Gln Phe Phe Val Thr Phe Phe Ser Cys Phe Leu Ser Leu Leu Leu Val 1285 1290 1295			3888
gct gct gtg gtt tgg aag atc aaa caa agt tgt tgg gcc tcc aga cgt Ala Ala Val Val Trp Lys Ile Lys Gln Ser Cys Trp Ala Ser Arg Arg 1300 1305 1310			3936
aga gag caa ctt ctt cga gag atg caa cag atg gcc agc cgt ccc ttt Arg Glu Gln Leu Leu Arg Glu Met Gln Gln Met Ala Ser Arg Pro Phe 1315 1320 1325			3984
gcc tct gta aat gtc gcc ttg gaa aca gat gag gag cct cct gat ctt Ala Ser Val Asn Val Ala Leu Glu Thr Asp Glu Glu Pro Pro Asp Leu 1330 1335 1340			4032
att ggg ggg agt ata aag act gtt ccc aaa ccc att gca ctg gag ccg Ile Gly Gly Ser Ile Lys Thr Val Pro Lys Pro Ile Ala Leu Glu Pro 1345 1350 1355 1360			4080
tgt ttt ggc aac aaa gcc gct gtc ctc tct gtg ttt gtg agg ctc cct Cys Phe Gly Asn Lys Ala Ala Val Leu Ser Val Phe Val Arg Leu Pro 1365 1370 1375			4128
cga ggc ctg ggt ggc atc cct cct cct ggg cag tca ggt ctt gct gtg Arg Gly Leu Gly Gly Ile Pro Pro Pro Gly Gln Ser Gly Leu Ala Val 1380 1385 1390			4176
gcc agc gcc ctg gtg gac att tct cag cag atg ccg ata gtg tac aag Ala Ser Ala Leu Val Asp Ile Ser Gln Gln Met Pro Ile Val Tyr Lys 1395 1400 1405			4224
gag aag tca gga gcc gtg aga aac cgg aag cag cag ccc cct gca cag Glu Lys Ser Gly Ala Val Arg Asn Arg Lys Gln Gln Pro Pro Ala Gln 1410 1415 1420			4272
cct ggg acc tgc atc tga Pro Gly Thr Cys Ile 1425			4290

<210> 14
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
 1 5 10 15
 Leu Met Ser Ala Gln Glu Ser Trp Ala
 20 25

<210> 15
 <211> 5
 <212> PRT
 <213> Bos taurus

<400> 15
 Lys Phe Glu Arg Gln
 1 5

<210> 16
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro
 1 5 10 15

<210> 17
 <211> 4
 <212> PRT
 <213> Rattus norvegicus

<400> 17
 Lys Asp Glu Leu
 1

<210> 18
 <211> 1272
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr
 1 5 10 15
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp
 20 25 30
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg
 35 40 45
 Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu
 50 55 60
 Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu Leu Leu Leu Pro Cys Glu
 65 70 75 80
 Ala Glu Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala
 85 90 95

Glu	Ala	Lys	Glu	Cys	Asp	Arg	Pro	Cys	Val	Asn	Gly	Gly	Arg	Cys	Asn	100	105	110
Pro	Gly	Thr	Gly	Gln	Cys	Val	Cys	Pro	Ala	Gly	Trp	Val	Gly	Glu	Gln	115	120	125
Cys	Gln	His	Cys	Gly	Gly	Arg	Phe	Arg	Leu	Thr	Gly	Ser	Ser	Gly	Phe	130	135	140
Val	Thr	Asp	Gly	Pro	Gly	Asn	Tyr	Lys	Tyr	Lys	Thr	Lys	Cys	Thr	Trp	145	150	155
Leu	Ile	Glu	Gly	Gln	Pro	Asn	Arg	Ile	Met	Arg	Leu	Arg	Phe	Asn	His	165	170	175
Phe	Ala	Thr	Glu	Cys	Ser	Trp	Asp	His	Leu	Tyr	Val	Tyr	Asp	Gly	Asp	180	185	190
Ser	Ile	Tyr	Ala	Pro	Leu	Val	Ala	Ala	Phe	Ser	Gly	Leu	Ile	Val	Pro	195	200	205
Glu	Arg	Asp	Gly	Asn	Glu	Thr	Val	Pro	Glu	Val	Val	Ala	Thr	Ser	Gly	210	215	220
Tyr	Ala	Leu	Leu	His	Phe	Phe	Ser	Asp	Ala	Ala	Tyr	Asn	Leu	Thr	Gly	225	230	235
Phe	Asn	Ile	Thr	Tyr	Ser	Phe	Asp	Met	Cys	Pro	Asn	Asn	Cys	Ser	Gly	245	250	255
Arg	Gly	Glu	Cys	Lys	Ile	Ser	Asn	Ser	Ser	Glu	Thr	Val	Glu	Cys	Glu	260	265	270
Cys	Ser	Glu	Asn	Trp	Lys	Gly	Glu	Ala	Cys	Asp	Ile	Pro	His	Cys	Thr	275	280	285
Asp	Asn	Cys	Gly	Phe	Pro	His	Arg	Gly	Ile	Cys	Asn	Ser	Ser	Asp	Val	290	295	300
Arg	Gly	Cys	Ser	Cys	Phe	Ser	Asp	Trp	Gln	Gly	Pro	Gly	Cys	Ser	Val	305	310	315
Pro	Val	Pro	Ala	Asn	Gln	Ser	Phe	Trp	Thr	Arg	Glu	Glu	Tyr	Ser	Asn	325	330	335
Leu	Lys	Leu	Pro	Arg	Ala	Ser	His	Lys	Ala	Val	Val	Asn	Gly	Asn	Ile	340	345	350
Met	Trp	Val	Val	Gly	Gly	Tyr	Met	Phe	Asn	His	Ser	Asp	Tyr	Asn	Met	355	360	365
Val	Leu	Ala	Tyr	Asp	Leu	Ala	Ser	Arg	Glu	Trp	Leu	Pro	Leu	Asn	Arg	370	375	380
Ser	Val	Asn	Asn	Val	Val	Val	Arg	Tyr	Gly	His	Ser	Leu	Ala	Leu	Tyr	385	390	395
Lys	Asp	Lys	Ile	Tyr	Met	Tyr	Gly	Gly	Lys	Ile	Asp	Pro	Thr	Gly	Asn	405	410	415
Val	Thr	Asn	Glu	Leu	Arg	Val	Phe	His	Ile	His	Asn	Glu	Ser	Trp	Val	420	425	430
Leu	Leu	Thr	Pro	Lys	Ala	Lys	Glu	Gln	Tyr	Ala	Val	Val	Gly	His	Ser	435	440	445
Ala	His	Ile	Val	Thr	Leu	Lys	Asn	Gly	Arg	Val	Val	Met	Leu	Val	Ile	450	455	460
Phe	Gly	His	Cys	Pro	Leu	Tyr	Gly	Tyr	Ile	Ser	Asn	Val	Gln	Glu	Tyr	465	470	475
Asp	Leu	Asp	Lys	Asn	Thr	Trp	Ser	Ile	Leu	His	Thr	Gln	Gly	Ala	Leu	485	490	495
Val	Gln	Gly	Gly	Tyr	Gly	His	Ser	Ser	Val	Tyr	Asp	His	Arg	Thr	Arg	500	505	510
Ala	Leu	Tyr	Val	His	Gly	Gly	Tyr	Lys	Ala	Phe	Ser	Ala	Asn	Lys	Tyr	515	520	525
Arg	Leu	Ala	Asp	Asp	Leu	Tyr	Arg	Tyr	Asp	Val	Asp	Thr	Gln	Met	Trp	530	535	540
Thr	Ile	Leu	Lys	Asp	Ser	Arg	Phe	Phe	Arg	Tyr	Leu	His	Thr	Ala	Val			

545					550					555				560	
Ile	Val	Ser	Gly	Thr	Met	Leu	Val	Phe	Gly	Gly	Asn	Thr	His	Asn	Asp
				565					570					575	
Thr	Ser	Met	Ser	His	Gly	Ala	Lys	Cys	Phe	Ser	Ser	Asp	Phe	Met	Ala
			580					585					590		
Tyr	Asp	Ile	Ala	Cys	Asp	Arg	Trp	Ser	Val	Leu	Pro	Arg	Pro	Asp	Leu
		595					600					605			
His	His	Asp	Val	Asn	Arg	Phe	Gly	His	Ser	Ala	Val	Leu	His	Asn	Ser
	610					615					620				
Thr	Met	Tyr	Val	Phe	Gly	Gly	Phe	Asn	Ser	Leu	Leu	Leu	Ser	Asp	Ile
625					630					635					640
Leu	Val	Phe	Thr	Ser	Glu	Gln	Cys	Asp	Ala	His	Arg	Ser	Glu	Ala	Ala
				645					650					655	
Cys	Leu	Ala	Ala	Gly	Pro	Gly	Ile	Arg	Cys	Val	Trp	Asn	Thr	Gly	Ser
			660					665					670		
Ser	Gln	Cys	Ile	Ser	Trp	Ala	Leu	Ala	Thr	Asp	Glu	Gln	Glu	Glu	Lys
		675					680					685			
Leu	Lys	Ser	Glu	Cys	Phe	Ser	Lys	Arg	Thr	Leu	Asp	His	Asp	Arg	Cys
	690					695					700				
Asp	Gln	His	Thr	Asp	Cys	Tyr	Ser	Cys	Thr	Ala	Asn	Thr	Asn	Asp	Cys
705					710					715					720
His	Trp	Cys	Asn	Asp	His	Cys	Val	Pro	Arg	Asn	His	Ser	Cys	Ser	Glu
			725						730					735	
Gly	Gln	Ile	Ser	Ile	Phe	Arg	Tyr	Glu	Asn	Cys	Pro	Lys	Asp	Asn	Pro
			740					745					750		
Met	Tyr	Tyr	Cys	Asn	Lys	Lys	Thr	Ser	Cys	Arg	Ser	Cys	Ala	Leu	Asp
		755					760					765			
Gln	Asn	Cys	Gln	Trp	Glu	Pro	Arg	Asn	Gln	Glu	Cys	Ile	Ala	Leu	Pro
	770					775					780				
Glu	Asn	Ile	Cys	Gly	Ile	Gly	Trp	His	Leu	Val	Gly	Asn	Ser	Cys	Leu
785					790					795					800
Lys	Ile	Thr	Thr	Ala	Lys	Glu	Asn	Tyr	Asp	Asn	Ala	Lys	Leu	Phe	Cys
				805					810					815	
Arg	Asn	His	Asn	Ala	Leu	Leu	Ala	Ser	Leu	Thr	Thr	Gln	Lys	Lys	Val
			820					825					830		
Glu	Phe	Val	Leu	Lys	Gln	Leu	Arg	Ile	Met	Gln	Ser	Ser	Gln	Ser	Met
	835						840					845			
Ser	Lys	Leu	Thr	Leu	Thr	Pro	Trp	Val	Gly	Leu	Arg	Lys	Ile	Asn	Val
	850					855					860				
Ser	Tyr	Trp	Cys	Trp	Glu	Asp	Met	Ser	Pro	Phe	Thr	Asn	Ser	Leu	Leu
865					870					875					880
Gln	Trp	Met	Pro	Ser	Glu	Pro	Ser	Asp	Ala	Gly	Phe	Cys	Gly	Ile	Leu
				885					890					895	
Ser	Glu	Pro	Ser	Thr	Arg	Gly	Leu	Lys	Ala	Ala	Thr	Cys	Ile	Asn	Pro
			900					905					910		
Leu	Asn	Gly	Ser	Val	Cys	Glu	Arg	Pro	Ala	Asn	His	Ser	Ala	Lys	Gln
		915					920					925			
Cys	Arg	Thr	Pro	Cys	Ala	Leu	Arg	Thr	Ala	Cys	Gly	Asp	Cys	Thr	Ser
	930					935					940				
Gly	Ser	Ser	Glu	Cys	Met	Trp	Cys	Ser	Asn	Met	Lys	Gln	Cys	Val	Asp
945					950					955					960
Ser	Asn	Ala	Tyr	Val	Ala	Ser	Phe	Pro	Phe	Gly	Gln	Cys	Met	Glu	Trp
				965					970					975	
Tyr	Thr	Met	Ser	Thr	Cys	Pro	Pro	Glu	Asn	Cys	Ser	Gly	Tyr	Cys	Thr
			980					985					990		
Cys	Ser	His	Cys	Leu	Glu	Gln	Pro	Gly	Cys	Gly	Trp	Cys	Thr	Asp	Pro

995 1000 1005
 Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro
 1010 1015 1020
 Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro
 1025 1030 1035 1040
 Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser
 1045 1050 1055
 Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile
 1060 1065 1070
 Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His
 1075 1080 1085
 Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly
 1090 1095 1100
 Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr
 1105 1110 1115 1120
 Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu
 1125 1130 1135
 Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg
 1140 1145 1150
 Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser
 1155 1160 1165
 Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala
 1170 1175 1180
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser
 1185 1190 1195 1200
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly
 1205 1210 1215
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys
 1220 1225 1230
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His
 1235 1240 1245
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile
 1250 1255 1260
 Lys Ile Gln Val Gln Thr Glu Gln
 1265 1270

<210> 19
 <211> 3819
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(3816)

<400> 19
 atg gtg gcc gca gcg gcg gca act gag gca agg ctg agg agg agg acg 48
 Met Val Ala Ala Ala Ala Ala Thr Glu Ala Arg Leu Arg Arg Arg Thr
 1 5 10 15
 gcg gcg acg gca gcg ctc gcg ggc agg agc ggc ggg ccg cac tgg gac 96
 Ala Ala Thr Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Trp Asp
 20 25 30
 tgg gac gtg acc agg gct ggg agg ccg ggg ctg ggg gcc ggg ctg cgc 144
 Trp Asp Val Thr Arg Ala Gly Arg Pro Gly Leu Gly Ala Gly Leu Arg
 35 40 45

ctc ccg cgg ctg ctg tct cca ccg ctg cgg cca ccg ctg ctg ctg ctg	192
Leu Pro Arg Leu Leu Ser Pro Pro Leu Arg Pro Arg Leu Leu Leu Leu	
50 55 60	
ctg ttg ttg ctc ccg ccg ccg ctg ttg ctg ctg ctg ctg ccc tgt gag	240
Leu Leu Leu Leu Pro Pro Pro Leu Leu Leu Leu Leu Leu Pro Cys Glu	
65 70 75 80	
gcc gag gcc gcg gcg gcg gcg gcg gcg gtg tgc ggc tca gcc gca gcc	288
Ala Glu Ala Ala Ala Ala Ala Ala Ala Val Ser Gly Ser Ala Ala Ala	
85 90 95	
gag gcc aag gaa tgt gac cgg ccc tgt gtc aac ggc ggt cgc tgc aac	336
Glu Ala Lys Glu Cys Asp Arg Pro Cys Val Asn Gly Gly Arg Cys Asn	
100 105 110	
cct ggc acc ggc cag tgc gtc tgc ccc gcc ggc tgg gtg ggc gag caa	384
Pro Gly Thr Gly Gln Cys Val Cys Pro Ala Gly Trp Val Gly Glu Gln	
115 120 125	
tgc cag cac tgc ggg ggc cgc ttc aga cta act gga tct tct ggg ttt	432
Cys Gln His Cys Gly Gly Arg Phe Arg Leu Thr Gly Ser Ser Gly Phe	
130 135 140	
gtg aca gat gga cct gga aat tat aaa tac aaa acg aag tgc acg tgg	480
Val Thr Asp Gly Pro Gly Asn Tyr Lys Tyr Lys Thr Lys Cys Thr Trp	
145 150 155 160	
ctc att gaa gga cag cca aat aga ata atg aga ctt cgt ttc aat cat	528
Leu Ile Glu Gly Gln Pro Asn Arg Ile Met Arg Leu Arg Phe Asn His	
165 170 175	
ttt gct aca gag tgt agt tgg gac cat tta tat gtt tat gat ggg gac	576
Phe Ala Thr Glu Cys Ser Trp Asp His Leu Tyr Val Tyr Asp Gly Asp	
180 185 190	
tca att tat gca ccg cta gtt gct gca ttt agt ggc ctc att gtt cct	624
Ser Ile Tyr Ala Pro Leu Val Ala Ala Phe Ser Gly Leu Ile Val Pro	
195 200 205	
gag aga gat ggc aat gag act gtc cct gag gtt gtt gcc aca tca ggt	672
Glu Arg Asp Gly Asn Glu Thr Val Pro Glu Val Val Ala Thr Ser Gly	
210 215 220	
tat gcc ttg ctg cat ttt ttt agt gat gct gct tat aat ttg act gga	720
Tyr Ala Leu Leu His Phe Phe Ser Asp Ala Ala Tyr Asn Leu Thr Gly	
225 230 235 240	
ttt aat att act tac agt ttt gat atg tgt cca aat aac tgc tca ggc	768
Phe Asn Ile Thr Tyr Ser Phe Asp Met Cys Pro Asn Asn Cys Ser Gly	
245 250 255	
cga gga gag tgt aag atc agt aat agc agc gaa act gtt gaa tgt gaa	816
Arg Gly Glu Cys Lys Ile Ser Asn Ser Ser Glu Thr Val Glu Cys Glu	
260 265 270	

tgt tct gaa aac tgg aaa ggt gaa gca tgt gac att cct cac tgt aca Cys Ser Glu Asn Trp Lys Gly Glu Ala Cys Asp Ile Pro His Cys Thr 275 280 285	864
gac aac tgt ggt ttt cct cat cga ggc atc tgc aat tca agt gat gtc Asp Asn Cys Gly Phe Pro His Arg Gly Ile Cys Asn Ser Ser Asp Val 290 295 300	912
aga gga tgc tcc tgc ttc tca gac tgg cag ggt cct gga tgt tca gtt Arg Gly Cys Ser Cys Phe Ser Asp Trp Gln Gly Pro Gly Cys Ser Val 305 310 315 320	960
cct gta cca gct aac cag tca ttt tgg act cga gag gaa tat tct aac Pro Val Pro Ala Asn Gln Ser Phe Trp Thr Arg Glu Glu Tyr Ser Asn 325 330 335	1008
tta aag ctc ccc aga gca tct cat aaa gct gtg gtc aat gga aac att Leu Lys Leu Pro Arg Ala Ser His Lys Ala Val Val Asn Gly Asn Ile 340 345 350	1056
atg tgg gtt gtt gga gga tat atg ttc aac cac tca gat tat aac atg Met Trp Val Val Gly Gly Tyr Met Phe Asn His Ser Asp Tyr Asn Met 355 360 365	1104
gtt cta gcg tat gac ctt gct tct agg gag tgg ctt cca cta aac cgt Val Leu Ala Tyr Asp Leu Ala Ser Arg Glu Trp Leu Pro Leu Asn Arg 370 375 380	1152
tct gtg aac aat gtg gtt gtt aga tat ggt cat tct ttg gca tta tac Ser Val Asn Asn Val Val Val Arg Tyr Gly His Ser Leu Ala Leu Tyr 385 390 395 400	1200
aag gat aaa att tac atg tat gga gga aaa att gat cca act ggg aat Lys Asp Lys Ile Tyr Met Tyr Gly Gly Lys Ile Asp Pro Thr Gly Asn 405 410 415	1248
gtg acc aat gag ttg aga gtt ttt cac att cat aat gag tca tgg gtg Val Thr Asn Glu Leu Arg Val Phe His Ile His Asn Glu Ser Trp Val 420 425 430	1296
ttg ttg acc cct aag gca aag gag cag tat gca gtg gtt ggg cac tct Leu Leu Thr Pro Lys Ala Lys Glu Gln Tyr Ala Val Val Gly His Ser 435 440 445	1344
gca cac att gtt aca ctg aag aat ggc cga gtg gtc atg ctg gtc atc Ala His Ile Val Thr Leu Lys Asn Gly Arg Val Val Met Leu Val Ile 450 455 460	1392
ttt ggt cac tgc cct ctc tat gga tat ata agc aat gtg cag gaa tat Phe Gly His Cys Pro Leu Tyr Gly Tyr Ile Ser Asn Val Gln Glu Tyr 465 470 475 480	1440
gat ttg gat aag aac aca tgg agt ata tta cac acc cag ggt gcc ctt Asp Leu Asp Lys Asn Thr Trp Ser Ile Leu His Thr Gln Gly Ala Leu 485 490 495	1488
gtg caa ggg ggt tac ggc cat agc agt gtt tac gac cat agg acc agg	1536

Val	Gln	Gly	Gly	Tyr	Gly	His	Ser	Ser	Val	Tyr	Asp	His	Arg	Thr	Arg	
		500						505					510			
gcc	cta	tac	gtt	cat	ggt	ggc	tac	aag	gct	ttc	agt	gcc	aat	aag	tac	1584
Ala	Leu	Tyr	Val	His	Gly	Gly	Tyr	Lys	Ala	Phe	Ser	Ala	Asn	Lys	Tyr	
		515					520					525				
cgg	ctt	gca	gat	gat	ctc	tac	cga	tat	gat	gtg	gat	acc	cag	atg	tgg	1632
Arg	Leu	Ala	Asp	Asp	Leu	Tyr	Arg	Tyr	Asp	Val	Asp	Thr	Gln	Met	Trp	
		530				535					540					
acc	att	ctt	aag	gac	agc	cga	ttt	ttc	cgt	tac	ttg	cac	aca	gct	gtg	1680
Thr	Ile	Leu	Lys	Asp	Ser	Arg	Phe	Phe	Arg	Tyr	Leu	His	Thr	Ala	Val	
545					550				555						560	
ata	gtg	agt	gga	acc	atg	ctg	gtg	ttt	ggg	gga	aac	aca	cac	aat	gac	1728
Ile	Val	Ser	Gly	Thr	Met	Leu	Val	Phe	Gly	Gly	Asn	Thr	His	Asn	Asp	
			565					570						575		
aca	tct	atg	agc	cat	ggc	gcc	aaa	tgc	ttc	tct	tca	gat	ttc	atg	gcc	1776
Thr	Ser	Met	Ser	His	Gly	Ala	Lys	Cys	Phe	Ser	Ser	Asp	Phe	Met	Ala	
		580						585					590			
tat	gac	att	gcc	tgt	gac	cgc	tgg	tca	gtg	ctt	ccc	aga	cct	gat	ctc	1824
Tyr	Asp	Ile	Ala	Cys	Asp	Arg	Trp	Ser	Val	Leu	Pro	Arg	Pro	Asp	Leu	
		595					600					605				
cac	cat	gat	gtc	aac	aga	ttt	ggc	cat	tca	gca	gtc	tta	cac	aac	agc	1872
His	His	Asp	Val	Asn	Arg	Phe	Gly	His	Ser	Ala	Val	Leu	His	Asn	Ser	
	610					615					620					
acc	atg	tat	gtg	ttc	ggt	ggt	ttc	aat	agt	ctc	ctc	ctc	agc	gac	atc	1920
Thr	Met	Tyr	Val	Phe	Gly	Gly	Phe	Asn	Ser	Leu	Leu	Leu	Ser	Asp	Ile	
625					630					635					640	
ctg	gta	ttc	acc	tcg	gaa	cag	tgt	gat	gcg	cat	cgg	agt	gaa	gcc	gct	1968
Leu	Val	Phe	Thr	Ser	Glu	Gln	Cys	Asp	Ala	His	Arg	Ser	Glu	Ala	Ala	
				645					650					655		
tgt	tta	gca	gca	gga	cct	ggt	att	cgg	tgt	gtg	tgg	aac	aca	ggg	tcg	2016
Cys	Leu	Ala	Ala	Gly	Pro	Gly	Ile	Arg	Cys	Val	Trp	Asn	Thr	Gly	Ser	
		660						665					670			
tct	cag	tgt	atc	tcg	tgg	gcg	ctg	gca	act	gat	gaa	caa	gaa	gaa	aag	2064
Ser	Gln	Cys	Ile	Ser	Trp	Ala	Leu	Ala	Thr	Asp	Glu	Gln	Glu	Glu	Lys	
		675					680					685				
tta	aaa	tca	gaa	tgt	ttt	tcc	aaa	aga	act	ctt	gac	cat	gac	aga	tgt	2112
Leu	Lys	Ser	Glu	Cys	Phe	Ser	Lys	Arg	Thr	Leu	Asp	His	Asp	Arg	Cys	
	690						695				700					
gac	cag	cac	aca	gat	tgt	tac	agc	tgt	aca	gcc	aac	acc	aat	gac	tgc	2160
Asp	Gln	His	Thr	Asp	Cys	Tyr	Ser	Cys	Thr	Ala	Asn	Thr	Asn	Asp	Cys	
705					710				715						720	
cac	tgg	tgc	aat	gac	cat	tgt	gtc	ccc	agg	aac	cac	agc	tgc	tca	gaa	2208
His	Trp	Cys	Asn	Asp	His	Cys	Val	Pro	Arg	Asn	His	Ser	Cys	Ser	Glu	

725								730				735				
ggc	cag	atc	tcc	att	ttt	agg	tat	gag	aat	tgc	ccc	aag	gat	aac	ccc	2256
Gly	Gln	Ile	Ser	Ile	Phe	Arg	Tyr	Glu	Asn	Cys	Pro	Lys	Asp	Asn	Pro	
740								745				750				
atg	tac	tac	tgt	aac	aag	aag	acc	agc	tgc	agg	agc	tgt	gcc	ctg	gac	2304
Met	Tyr	Tyr	Cys	Asn	Lys	Lys	Thr	Ser	Cys	Arg	Ser	Cys	Ala	Leu	Asp	
755								760				765				
cag	aac	tgc	cag	tgg	gag	ccc	cgg	aat	cag	gag	tgc	att	gcc	ctg	ccc	2352
Gln	Asn	Cys	Gln	Trp	Glu	Pro	Arg	Asn	Gln	Glu	Cys	Ile	Ala	Leu	Pro	
770								775				780				
gaa	aat	atc	tgt	ggc	att	ggc	tgg	cat	ttg	gtt	gga	aac	tca	tgt	ttg	2400
Glu	Asn	Ile	Cys	Gly	Ile	Gly	Trp	His	Leu	Val	Gly	Asn	Ser	Cys	Leu	
785								790				795				800
aaa	att	act	act	gcc	aag	gag	aat	tat	gac	aat	gct	aaa	ttg	ttc	tgt	2448
Lys	Ile	Thr	Thr	Ala	Lys	Glu	Asn	Tyr	Asp	Asn	Ala	Lys	Leu	Phe	Cys	
805								810				815				
agg	aac	cac	aat	gcc	ctt	ttg	gct	tct	ctt	aca	acc	cag	aag	aag	gta	2496
Arg	Asn	His	Asn	Ala	Leu	Leu	Ala	Ser	Leu	Thr	Thr	Gln	Lys	Lys	Val	
820								825				830				
gaa	ttt	gtc	ctt	aag	cag	ctg	cga	ata	atg	cag	tca	tct	cag	agc	atg	2544
Glu	Phe	Val	Leu	Lys	Gln	Leu	Arg	Ile	Met	Gln	Ser	Ser	Gln	Ser	Met	
835								840				845				
tcc	aag	ctc	acc	tta	acc	cca	tgg	gtc	ggc	ctt	cgg	aag	atc	aat	gtg	2592
Ser	Lys	Leu	Thr	Leu	Thr	Pro	Trp	Val	Gly	Leu	Arg	Lys	Ile	Asn	Val	
850								855				860				
tcc	tac	tgg	tgc	tgg	gaa	gat	atg	tcc	cca	ttt	aca	aat	agt	tta	cta	2640
Ser	Tyr	Trp	Cys	Trp	Glu	Asp	Met	Ser	Pro	Phe	Thr	Asn	Ser	Leu	Leu	
865								870				875				880
cag	tgg	atg	ccg	tct	gag	ccc	agt	gat	gct	gga	ttc	tgt	gga	att	tta	2688
Gln	Trp	Met	Pro	Ser	Glu	Pro	Ser	Asp	Ala	Gly	Phe	Cys	Gly	Ile	Leu	
885								890				895				
tca	gaa	ccc	agt	act	cgg	gga	ctg	aag	gct	gca	acc	tgc	atc	aac	cca	2736
Ser	Glu	Pro	Ser	Thr	Arg	Gly	Leu	Lys	Ala	Ala	Thr	Cys	Ile	Asn	Pro	
900								905				910				
ctc	aat	ggt	agt	gtc	tgt	gaa	agg	cct	gca	aac	cac	agt	gct	aag	cag	2784
Leu	Asn	Gly	Ser	Val	Cys	Glu	Arg	Pro	Ala	Asn	His	Ser	Ala	Lys	Gln	
915								920				925				
tgc	cgg	aca	cca	tgt	gcc	ttg	agg	aca	gca	tgt	gga	gat	tgc	acc	agc	2832
Cys	Arg	Thr	Pro	Cys	Ala	Leu	Arg	Thr	Ala	Cys	Gly	Asp	Cys	Thr	Ser	
930								935				940				
ggc	agc	tct	gag	tgc	atg	tgg	tgc	agc	aac	atg	aag	cag	tgt	gtg	gac	2880
Gly	Ser	Ser	Glu	Cys	Met	Trp	Cys	Ser	Asn	Met	Lys	Gln	Cys	Val	Asp	
945								950				955				960

tcc aat gcc tat gtg gcc tcc ttc cct ttt ggc cag tgt atg gaa tgg	2928
Ser Asn Ala Tyr Val Ala Ser Phe Pro Phe Gly Gln Cys Met Glu Trp	
965 970 975	
tat acg atg agc acc tgc ccc cct gaa aat tgt tca ggc tac tgt acc	2976
Tyr Thr Met Ser Thr Cys Pro Pro Glu Asn Cys Ser Gly Tyr Cys Thr	
980 985 990	
tgt agt cat tgc ttg gag caa cca ggc tgt ggc tgg tgt act gat ccc	3024
Cys Ser His Cys Leu Glu Gln Pro Gly Cys Gly Trp Cys Thr Asp Pro	
995 1000 1005	
agc aat act ggc aaa ggg aaa tgc ata gag ggt tcc tat aaa gga cca	3072
Ser Asn Thr Gly Lys Gly Lys Cys Ile Glu Gly Ser Tyr Lys Gly Pro	
1010 1015 1020	
gtg aag atg cct tcg caa gcc cct aca gga aat ttc tat cca cag ccc	3120
Val Lys Met Pro Ser Gln Ala Pro Thr Gly Asn Phe Tyr Pro Gln Pro	
1025 1030 1035 1040	
ctg ctc aat tcc agc atg tgt cta gag gac agc aga tac aac tgg tct	3168
Leu Leu Asn Ser Ser Met Cys Leu Glu Asp Ser Arg Tyr Asn Trp Ser	
1045 1050 1055	
ttc att cac tgt cca gct tgc caa tgc aac ggc cac agt aaa tgc atc	3216
Phe Ile His Cys Pro Ala Cys Gln Cys Asn Gly His Ser Lys Cys Ile	
1060 1065 1070	
aat cag agc atc tgt gag aag tgt gag aac ctg acc aca ggc aag cac	3264
Asn Gln Ser Ile Cys Glu Lys Cys Glu Asn Leu Thr Thr Gly Lys His	
1075 1080 1085	
tgc gag acc tgc ata tct ggc ttc tac ggt gat ccc acc aat gga ggg	3312
Cys Glu Thr Cys Ile Ser Gly Phe Tyr Gly Asp Pro Thr Asn Gly Gly	
1090 1095 1100	
aaa tgt cag cca tgc aag tgc aat ggg cac gcg tct ctg tgc aac acc	3360
Lys Cys Gln Pro Cys Lys Cys Asn Gly His Ala Ser Leu Cys Asn Thr	
1105 1110 1115 1120	
aac acg ggc aag tgc ttc tgc acc acc aag ggc gtc aag ggg gac gag	3408
Asn Thr Gly Lys Cys Phe Cys Thr Thr Lys Gly Val Lys Gly Asp Glu	
1125 1130 1135	
tgc cag cta tgt gag gta gaa aat cga tac caa gga aac cct ctc aga	3456
Cys Gln Leu Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg	
1140 1145 1150	
gga aca tgt tat tat act ctt ctt att gac tat cag ttc acc ttt agt	3504
Gly Thr Cys Tyr Tyr Thr Leu Leu Ile Asp Tyr Gln Phe Thr Phe Ser	
1155 1160 1165	
cta tcc cag gaa gat gat cgc tat tac aca gct atc aat ttt gtg gct	3552
Leu Ser Gln Glu Asp Asp Arg Tyr Tyr Thr Ala Ile Asn Phe Val Ala	
1170 1175 1180	

act cct gac gaa caa aac agg gat ttg gac atg ttc atc aat gcc tcc 3600
 Thr Pro Asp Glu Gln Asn Arg Asp Leu Asp Met Phe Ile Asn Ala Ser
 1185 1190 1195 1200

aag aat ttc aac ctc aac atc acc tgg gct gcc agt ttc tca gct gga 3648
 Lys Asn Phe Asn Leu Asn Ile Thr Trp Ala Ala Ser Phe Ser Ala Gly
 1205 1210 1215

acc cag gct gga gaa gag atg cct gtt gtt tca aaa acc aac att aag 3696
 Thr Gln Ala Gly Glu Glu Met Pro Val Val Ser Lys Thr Asn Ile Lys
 1220 1225 1230

gag tac aaa gat agt ttc tct aat gag aag ttt gat ttt cgc aac cac 3744
 Glu Tyr Lys Asp Ser Phe Ser Asn Glu Lys Phe Asp Phe Arg Asn His
 1235 1240 1245

cca aat atc act ttc ttt gtt tat gtc agt aat ttc acc tgg ccc atc 3792
 Pro Asn Ile Thr Phe Phe Val Tyr Val Ser Asn Phe Thr Trp Pro Ile
 1250 1255 1260

aaa att cag gtg caa act gaa caa tga 3819
 Lys Ile Gln Val Gln Thr Glu Gln
 1265 1270

<210> 20
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 20
 Cys Glu Val Glu Asn Arg Tyr Gln Gly Asn Pro Leu Arg Gly Thr Cys
 1 5 10 15
 Tyr

<210> 21
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 21
 Ala Ala Leu Ala Gly Arg Ser Gly Gly Pro His Cys
 1 5 10

<210> 22
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(4)
 <223> Xaa = Any Amino Acid
 <221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Gly, Ser, or Ala

<400> 22
 Gly Xaa Ser Xaa Xaa
 1 5

<210> 23
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (2)...(8)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, or Trp

<221> VARIANT
 <222> (10)...(29)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (30)...(30)
 <223> Xaa = Leu, Ile, Val, Met, Phe, Tyr, or Trp

<400> 23
 Asp Xaa Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly Gly Xaa
 20 25 30

<210> 24
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (3)...(4)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (6)...(6)
 <223> Xaa = Asp or Glu

<221> VARIANT
 <222> (9)...(9)
 <223> Xaa = Gly or Ser

<400> 24
 Ala Ala Xaa Xaa Gly Xaa Ser Gly Xaa Pro His
 1 5 10

<210> 25
 <211> 10

<212> DNA

<213> Homo sapiens

<400> 25

gggaagatgg